

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 01:26:57 ; Search time 3770 Seconds  
(without alignments)  
12035.175 Million cell updates/sec

Title: U67963

Perfect score: 1192

Sequence: 1 CCAGCCCGAAGGCGAGGTC.....CAAAAAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1102	92.4	1141	3	CR622559	full-length
2	909.2	76.3	1117	5	BM924140	AGENCOURT
3	886	74.3	961	5	BM924140	AGENCOURT
4	882.6	74.0	926	5	BM924140	AGENCOURT
5	863.4	72.4	1011	5	BUI182994	AGENCOURT
6	862	72.3	988	5	BUI185369	AGENCOURT
7	860.8	72.2	912	5	BUI501241	AGENCOURT
8	842.2	70.7	848	5	BUI541422	AGENCOURT
9	839.6	70.4	944	5	BQ591581	AGENCOURT
10	802.6	67.3	896	5	BQ591355	AGENCOURT
11	788.4	66.1	815	7	CN643629	ILLUMIGEN
12	783.4	65.7	878	5	BQ686359	AGENCOURT
13	772.2	64.8	916	5	BUI145364	AGENCOURT
14	768.8	64.5	806	4	B1758109	603023793
15	765.8	64.2	885	5	BUI169041	AGENCOURT
16	763.2	64.0	906	6	CD519322	AGENCOURT
17	760.4	63.8	869	4	B1490115	603031942
18	758.2	63.6	794	4	BM677640	UI-E-E01-
19	753.8	63.2	989	5	BX336911	BX336911
20	752.2	63.1	880	5	BQ690752	AGENCOURT
21	750	62.9	793	5	BX396586	AGENCOURT
22	748	62.8	916	4	BM047566	603628883
23	742.6	62.3	889	4	B1490635	603031942
24	740	62.1	781	5	BX414718	BX414718

25	736.8	61.8	855	4	BI869841	BI869841
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27	732.4	61.4	876	5	BUI185479	AGENCOURT
28	725.8	60.9	917	4	BG323643	602421923
29	715.8	60.1	856	5	BUI162613	AGENCOURT
30	713	59.8	867	5	BQ685155	AGENCOURT
31	712.4	59.8	947	5	BUI543714	AGENCOURT
32	704.4	59.1	978	5	BM926322	AGENCOURT
33	701	58.8	1160	4	BG323230	602421448
34	690.8	58.0	1107	3	AK028008	Mus muscu
35	689	57.8	689	4	BM794856	K-EST0076
36	683.4	57.3	946	4	BI821210	603034920
37	683	57.3	870	5	BQ686707	AGENCOURT
38	681.2	57.1	891	5	BUI163235	AGENCOURT
39	675.2	56.6	863	5	BQ687326	AGENCOURT
40	673.8	56.5	896	5	BQ684336	AGENCOURT
41	665.2	55.8	1134	4	BG034798	602325446
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44	659.8	55.4	709	2	BB856228	7f90f12.x
45	658.6	55.3	910	5	BUI839268	AGENCOURT

## ALIGNMENTS

RESULT 1	CR622559	1141 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSODI019YD19 of Placenta Cot 25-normalized				
DEFINITION	of Homo sapiens (human)				
ACCESSION	CR622559				
VERSION	CR622559.1	GI:50503366			
KEYWORDS	HTC; CNSLT cDNA				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1141)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr				

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="CSODI019YD19"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e-287;  
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Qy 1 CCAGCCGAAAGGAGGAGGCTCGGTCGGGAGAGGAGGCTCGGAGCTCGCTTCCTGCTGCC 60  
DB 40 CCAGCCGAAAGGAGGAGGCTCGGTCGGGAGAGGAGGCTCGGAGCTCGCTTCCTGCTGCC 99

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QY 121 GTGGTTGTGGAAATCAAAACGCCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 160 GTGGTTGTGGAAATCAAAACGCCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC 219
QY 181 ATGCCAGAGGAAGTTCCCCAGGCGGACCCCGCAGAGCATTCCTTACCAGGACCTCCCT 240
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QY 241 CACCTGGTCAATGCAGACGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300
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Db 400 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGTGTGTTTGGCCACGACCATTTGGCCAC 459
QY 421 GGACAGCGAAGGAGGAGGATGCTAGTGTCTGACTTCCAGTTTTCGTGAGGATGTG 480
Db 460 GGACAGCGAAGGAGGAGGATGCTAGTGTCTGACTTCCAGTTTTCGTGAGGATGTG 519
QY 481 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTCGGGCTTCCTGTCTTCTTCTGGCC 540
Db 520 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTCGGGCTTCCTGTCTTCTTCTGGCC 579
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Db 580 CACTTCATGGAGGCGCCATGCCATCTCTACGGCCGAGAGAGCGCGGCGCACTTCGCC 639
QY 601 GGCATGTTACTCATTTCCGCTCTGTTCTTGCCATCTGTAATCTGGAACAACTTCAAG 660
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QY 661 GTCTTTGCTGGGAAAGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGGCCCATCGAC 720
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Db 820 TGC CGGCGAGGCGCTGAAGTGTCTTGGCATCCAACTGCTGMAATGCCGTCTCAGGGTG 879
QY 841 GAGCGCGCTCCCCAAGCTGACTGTGCGCTTCTCTGTGCTCCAGGGCTCTGCGGATCGC 900
Db 880 GAGCGCGCTCCCCAAGCTGACTGTGCGCTTCTCTGTGCTCCAGGGCTCTGCGGATCGC 939
QY 901 CTATGTGACAGAAAGGGCCCTA CTTGCTCATGAGTTAGCCAAAGAGCAGCAGCAAGACT 960
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QY 961 CTCAGATTTATGAGTGGCTTACCATTCTTCCACAGGAGCTTCTTGAAGTCAACCAAC 1020
Db 1000 CTCAGATTTATGAGTGGCTTACCATTCTTCCACAGGAGCTTCTTGAAGTCAACCAAC 1059
QY 1021 TCCGCTTTCCATGAAATAAATGTTGGTCTCTCAAAGGACAGCCACGCGAGGAAGTCCG 1080
Db 1060 TCCGCTTTCCATGAAATAAATGTTGGTCTCTCAAAGGAGCTTCTCAAAGGAGTCCG 1119
QY 1081 TCCCAACCTGAAATGCAATTGGC 1102
Db 1120 TCCCAACCTGAAATGCAATTGGC 1141
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LOCUS
DEFINITION BX403703 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA009ZC10
5-PRIME, mRNA sequence.
ACCESSION BX403703
VERSION BX403703.2 GI:46929030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1117)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30643737.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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1..1117
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA009ZC10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 76.3%; Score 909.2; DB 5; Length 1117;
Best Local Similarity 93.6%; Pred. No. 2.5e-235;
Matches 970; Conservative 9; Mismatches 52; Indels 5; Gaps 3;
QY 158 CAGGACCTGAAGACCTTCCAGCATGCCAGGAAAGTTCCCCAGGCGGACCCCGCAGA 217
Db 84 CCGGACCTGAAGACCTTCCAGCATGCCAGGAAAGTTCCCCAGGCGGACCCCGCAGA 143
QY 218 GCATTCTCCAGGACCTCCCTCACCTGTCATGCGGACGAGTACCTCTTCTGCA 277
Db 144 GCATTCTCCAGGACCTCCCTCACCTGTCATGCGGACGAGTACCTCTTCTGCR 203
QY 278 GGTACTGGAACCCACAGGCACACCCAAAGGCCCTCATCTTGTGTCATGAGCCGGAG 337
Db 204 GGTACTGGAACCCACAGGCACACCCAAAGGCCCTCATCTTGTGTCATGAGCCGGAG 263
QY 338 AGCAGTGGCCGCTATGAAGAGCTGCTCGGATGCTGATGGGCTGGACCTGTGTTGT 397
Db 264 AGCAGTGGCCGCTATGAAGAGCTGCTCGGATGCTGATGGGCTGGACCTGTGTTGT 323
QY 398 TCGCCGAGGACCATGTTGGCCACGAGCAGAGCGGAGGAGATGGTAGTGTGACT 457
Db 324 TCGCCGAGGACCATGTTGGCCACGAGCAGAGCGGAGGAGATGGTAGTGTGACT 383
QY 458 TCCAGCTTTTCTGTCAGGAGTGTGTTGAGCATGTGGATTCCATGACAGAAAGACTACCCCTG 517
Db 384 TCCAGCTTTTCTGTCAGGAGTGTGTTGAGCATGTGGATTCCATGACAGAAAGACTACCCCTG 443
QY 518 GGCCTTCTGTTCTTCTTCTGGGCCACTCCCATGAGGAGCGGCATCGCCATCTCAAGCGCG 577
Db 444 GGCCTTCTGTTCTTCTTCTGGGCCACTCCCATGAGGAGCGGCATCGCCATCTCAAGCGCG 503
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QY 578 CAGAGAGCGCGGCACCTTCGCGGCATGGTACTCATTTTCGCTCTGGTCTTCTGGCAATC 637
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QY 638 CTGAATCTGCACAACTTTCAAGGTCCTTCTGCGGAAAGTGTCAACCTTGTGCTGCCAA 697
DB 564 CTGAATCTGCACAACTTTCAAGGTCCTTCTGCGGAAAGTGTCAACCTTGTGCTGCCAA 623
QY 698 ACTTGTCCCTCGCGGCCATCGACTCTCAGCGTCTCTCTCGGAATTAAGACAGAGGTCGACA 757
DB 624 ACTTGTCCCTCGCGGCCATCGACTCTCAGCGTCTCTCTCGGAATTAAGACAGAGGTCGACA 683
QY 758 TTATAACTCAGACCCCTGATCTGCGGCGCAGGCTCAAGGTGTGCTTTCGSCATCCCAAC 817
DB 684 TTATAACTCAGACCCCTGATCTGCGGCGCAGGCTCAAGGTGTGCTTTCGSCATCCCAAC 743
QY 818 TGCTGAATGCCCTCTCAGGGTGGAGCGCGCTCCCAAGCTGACTGTGCGCTTCCTGTC 877
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QY 938 TAGCCAAGAGCGCAGGACAGACTCTCAAGATTATGAAGGTGCTTACCATTGTCTCCACA 997
DB 864 TAGCCAAGAGCGCAGGACAGACTCTCAAGATTATGAAGGTGCTTACCATTGTCTCCACA 923
QY 998 AGGAGCTTCTGAAGTCAACACTCCGCTTTCATGAATAAACAATGAGGTCTCTC-AA 1056
DB 924 AGGAGCTTCTGAAGTCAACACTCCGCTTTCATGAATAAACAATGAGGTCTCTC-AA 983
QY 1057 AGGAGCGCAGCGGAGGAGTCCGTCCTCCACCTGATGCAATGCGCGGTCCCGGCTCA 1116
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QY 1177 AAAAAAAYAAAAA 1192
DB 1100 AAAAAAAYAAAAA 1115

RESULT 3
BM924140
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM924140
AGENCOURT 6630474 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760345
5', mRNA sequence.
BM924140
BM924140.1 GI:19374507
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM12807 row: d column: 10
High quality sequence stop: 719.

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/clone="IMAGE:5760345"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 74.3%; Score 886; DB 5; Length 961;
Best Local Similarity 98.8%; Pred. No. 4.8e-229;
Matches 908; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

263 AGTACCTCTTCTGAGGTACTTGGAAACCCACAGGCACACCCAGGCCCTCATCTTTGTGT 322
DB 25 AGTACCTCTTCTGAGGTACTTGGAAACCCACAGGCACACCCAGGCCCTCATCTTTGTGT 84
QY 323 CCCATGAGCGCGAGAGACAGTGGCGCTATGAAGAGTGGCTCGGATGTGATGGGCG 382
DB 85 CCCATGAGCGCGAGAGACAGTGGCGCTATGAAGAGTGGCTCGGATGTGATGGGCG 144
QY 383 TGGACCTGCTGCTTTCGCCACAGCATGTTGGCCACGGACAGAGCGAAGGGAGAGA 442
DB 145 TGGACCTGCTGCTTTCGCCACAGCATGTTGGCCACGGACAGAGCGAAGGGAGAGA 204
QY 443 TGGTAGTGTCTGACTTTCACCGTTTTCGTCAGGGATGTGTTGACGATGTGGATTCATGTC 502
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QY 503 AGAAGACTACCTGCGGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 562
DB 265 AGAAGACTACCTGCGGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 324
QY 563 CCATCCTCAGCGCGCAGAGAGCGCGGCCACTTTCGCCGCGCATGTACTCATTTTCGCTC 622
DB 325 CCATCCTCAGCGCGCAGAGAGCGCGGCCACTTTCGCCGCGCATGTACTCATTTTCGCTC 384
QY 623 TGGTTCCTTGGCAATCTCTGAATCTGCAACAACTTTTCAAGGTCTTTCGTCGAAAGTGTCTCA 682
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QY 683 ACCTTGTGTCGCAAACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 742
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DB 505 AGACAGAGGTGCATTTATTAATCTCAGACCCCTGATCTGCGGCGCAGGCTGAGGCTGT 564
QY 803 GTTTCGGCATCCAACTGCTGTAATGCCGTCTCAGGGGTGGAGCGCGCTCCCGCAAGCTGA 862
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Db |||||||
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Db |||||||
QY 805 TGTGGGTCTCTCAAAAGGACAGCCAGCGAGGAACCTGCGTCCCCACCCCTGAATGCATTGGG 864
QY 1102 CCGGTGCCCGGCTCATGTCTGGG-GGATGCGAGGAGGGGAAGGCGAGAGATGGCTTCTC 1160
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QY 865 NCGGTGCCCGGCTCATGTCTGGGNGGATGCGANGCAGGGGAAGGGCANAGATGGCTTCTC 924
QY 1161 AGATATGGCTTGCAAAAAA 1179
Db |||||||
QY 925 ANATATGGCTTGCGNNNNA 943

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DEFINITION BX396587 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1019YD19 5-PRIME, mRNA sequence.
ACCESSION BX396587
VERSION BX396587.2 GI:46876432
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Pollayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30621008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2061.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?g=CS0D1019CB10QP1&c=2061.r.
FEATURES
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1..926
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/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 74.0%; Score 882.6; DB 5; Length 926;
Best Local Similarity 99.1%; Pred. No. 3.9e-228;
Matches 879; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAGCCGAAAGCAGGGTCTGGGTGCGGGAGAGGGCTCGGAGCTGCGTCTCTGCTGCC 60
Db |||||||
QY 40 CCAGCCGAAAGCAGGGTCTGGGTGCGGGAGAGGGCTCGGAGCTGCGTCTCTGCTGCC 99
QY 61 TTGGGGCCGCCAGATAGGGAACAGCCGATTTCCCTGGTTCTGATTTCCAGGCTGTC 120
Db |||||||
QY 100 TTGGGGCCGCCAGATAGGGAACAGCCGATTTCCCTGGTTCTGATTTCCAGGCTGTC 159
QY 121 GTGGTTGTGGAATGCNAACGCCCAGCACATAATGGAAACAGGACCTTGAAGACCTTCCAGC 180
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Db |||||||
QY 160 GTGGTTGTGGAATGCNAACGCCCAGCACATAATGGAAACAGGACCTTGAAGACCTTCCAGC 219
QY 181 ATCCAGAGGAAAGTTCCCCAGCGGAGCCCGCAGAGCATTTCCCTACCAGGACTTCCTC 240
Db |||||||
QY 220 ATCCAGAGGAAAGTTCCCCAGCGGAGCCCGCAGAGCATTTCCCTACCAGGACTTCCTC 279
QY 241 CACTGGTCAATGACAGGAGACAGTACTCTTCTGAGGTAAGTCTGGAACCCACAGGACACA 300
Db |||||||
QY 280 CACTGGTCAATGACAGGAGACAGTACTCTTCTGAGGTAAGTCTGGAACCCACAGGACACA 339
QY 301 CCCAAGGCCCTCATCTTTGTGTCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360
Db |||||||
QY 340 CCCAAGGCCCTCATCTTTGTGTCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 399
QY 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGTGTGTGTGGCCCGACACCATGTTGGCCAC 420
Db |||||||
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QY 460 GGACAGAGCGAAGGGAGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTACAGGATGTG 519
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QY 820 TGCCGGCGCGGCTGAAGGTGCTTCGTCATCCCACTGCTGAATGCTGCTGCTCAGCGGTG 879
QY 841 GAGCGCGCCCTCCCAAGCTGACTGTGCGCCTTCTCTGCTGCTCAGCGGTG 887
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5', mRNA sequence.
ACCESSION BX396587
VERSION BX396587.1 GI:22676946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 1011)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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Location/Qualifiers

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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.4%; Score 863.4; DB 5; Length 1011;  
 Best Local Similarity 95.9%; Pred. No. 6.e-223;  
 Matches 929; Conservative 0; Mismatches 36; Indels 4; Gaps 4;

QY 1 CCAGCCGGAAGGCGAGGCTCGGGTCGGGAAGAGGGCTCGAGTGCCTTCCTGCTGCC 60  
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 DB 222 ATGCCAGAGGAAGTTCCCCAGGCGGACCCCGCAGAGCATTTCCCTACCGAGACCTCCCT 281  
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 988)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## FEATURES

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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.3%; Score 862; DB 5; Length 988;

Best Local Similarity 97.1%; Pred. No. 1.6e-222; Matches 951; Conservative 0; Mismatches 21; Indels 7; Gaps 7;									
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Qy	301	CCCAAGGCCCTCATCTTTGTGTCCTATGAGCGGAGACAGTGGCGCTATGAAGAG	360						
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Qy	421	GGACAGACGGAAGGGGAGAGATGTTAGTGTCTGACTTTCACGTTTTCGTGAGGATGTG	480						
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Qy	840	GGAGCGCG-CCCTCCCAAGCTGACTGT-GCCCTTCTGCTGCTCAGGGGCTCTGCCGAT	897						
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Qy	898	-CGCTATGTGACAGCAAGGGGCGCTA-CGTGCTCATGGAGTTAGCCAG-AGCCAGGAC	954						
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BU501241  
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DEFINITION AGENCOURT 8877702 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:6337918  
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VERSION BU501241.1 GI:22803436  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LICM9530 row: e column: 23  
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EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. |"

ORIGIN

Query Match	72.2%;	Score	860.8;	DB	5;	Length	912;
Best Local Similarity	99.4%;	Pred. No.	3.3e-222;				
Matches	884;	Conservative	0;	Mismatches	3;	Indels	2;
Gaps	2;						
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Db	315	CCCAAGGCCCTCATCTTTGTGTCCTATGAGCGGAGACAGTGGCGCTATGAAGAG	374				



QY 361 CTGGCTCGGATCTGATGGGGTGGACCTGCTGGTGGTTCGCCACGACATGTTGGCCAC 420  
 Db 375 CTGGCTCGGATCTGATGGGGTGGACCTGCTGGTGGTTCGCCACGACATGTTGGCCAC 434  
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## RESULT 8

BUS41422 848 bp mRNA linear EST 13-SEP-2002  
 LOCUS AGENCOURT\_10333378 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6573101  
 DEFINITION 5', mRNA sequence.

ACCESSION BUS41422  
 VERSION BUS41422.1 GI:22851863  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 848)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

## AUTHORS

Contact: Robert Strausberg, Ph.D.

## TITLE

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

## JOURNAL

Tissue Procurement: DCTD/DRP  
 cDNA Library Prepared by: Rubin Laboratory  
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

## COMMENT

<http://image.llnl.gov>

## FEATURES

## source

High quality sequence stop: 729.  
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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.7%; Score 842.2; DB 5; Length 848;  
 Best Local Similarity 99.5%; Pred. No. 3.6e-217;  
 Matches 844; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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BQ691581
LOCUS
DEFINITION BQ691581 944 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8341900 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249076
5', mRNA sequence.
ACCESSION BQ691581
VERSION BQ691581.1 GI:21816897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 944)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2389 row: p column: 05
High quality sequence stop: 751.
Location/Qualifiers
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/tissue_type="ductal carcinoma, cell line"
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/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 70.4%; Score 839.6; DB 5; Length 944;
Best Local Similarity 97.9%; Pred. No. 1.9e-215;
Matches 872; Conservative 0; Mismatches 15; Indels 4; Gaps 2;
QY 1 CCAGCCCGAAGGCGAGGCTGGGTGCGGGAAGAGGGCTCGAGGTGCTTCCTGCTGCC 60
DB 6 CCAGCCCGAAGGCGAGGCTGGGTGCGGGAAGAGGGCTCGAGGTGCTTCCTGCTGCC 65
QY 61 TTGGGGCCCGCAGATGAGGAAACAGCCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC 120
DB 66 TTGGGGCCCGCAGATGAGGAAACAGCCCGATTTGCTGGTTCTGATTTCTCAGGCTGTC 125
QY 121 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGAGACCTGAAGACCTTCCAGC 180
DB 126 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGAGACCTTGAAGACCTTCCAGC 185
QY 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTTCCCTACAGGACCTCCCT 240
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QY 241 CACCTGGTCAATGCGAGCGACAGTACCTCTTCTGCGAGTACTGGAAACCCACAGGACACA 300
DB 246 CACCTGGTCAATGCGAGCGACAGTACCTCTTCTGCGAGTACTGGAAACCCACAGGACACA 305
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QY 361 CTGGCTCGATGCTGATGAGGGCTGGACCTGCTGGTGTTCGCCACAGACCATGTTGGCCAC 420
DB 366 CTGGCTCGATGCTGATGAGGGCTGGACCTGCTGGTGTTCGCCACAGACCATGTTGGCCAC 425
QY 421 GGACAGAGCGAAGGGGAGAGATGCTGTGACTTCCACGCTTTTCGTCAGGATGTG 480
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DB 666 GTCCTTCTCGAAGTGCTCAACTTGTGTGTCGCAAACTTGTCCCTCGGGCCCATCGAC 725
QY 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATTAACAGACCCCTGATC 780
DB 726 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGACATTTATTAACAGACCCCTGATC 785
QY 781 TGCGGGCAGGGCTGAAGTGTGCTTCGGCATCCAACTGCTGAATGCTCTCACGGGTG 840
DB 786 TGCGGGCAGGGCTGAAGTGTGCTTCGGCATCCAACTGCTGAATGCTCTCACGGGTG 845
QY 841 GAGCGCG-CCCTCCCAAGCTGACTGTG-CCCTTCCTGCTGCTCCAGG 887
DB 846 TGGAGCGCGCCCTCCCAAGCTGACTGTGCGCCCTTCCTGCTGCTCCAANG 896
BQ691355 896 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8340818 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249249
5', mRNA sequence.
BQ691355
VERSION BQ691355.1 GI:21816671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 896)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2390 row: g column: 10
High quality sequence stop: 745.
Location/Qualifiers
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/tissue\_type="ductal carcinoma, cell line"  
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 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 67.3%; Score 802.6; DB 5; Length 896;  
 Best Local Similarity 98.8%; Pred. No. 2.1e-206;  
 Matches 819; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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 Qy 61 TTGGGGCCGCGCAGATGAGGAAACAGCCCGATTTGCCCTGTTCTGATTTCCAGGCTGTC 120  
 Db |||||  
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 Qy 121 GTGGTTGTGGAATCAAAACGCGCAGCACATAATGGAACAGGACCTTGAGACCTTCCAGC 180  
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 125 GTGGTTGTGGAATCAAAACGCGCAGCACATAATGGAACAGGACCTTGAGACCTTCCAGC 184  
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 Db |||||  
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 245 CACCTGGTCAATGCAGAGGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGACACA 304  
 Qy 301 CCCAAGGCCCTCATCTTTGTGTCCATGAGCCGAGAGCAGTGGCGCGTATGAAGAG 360  
 Db |||||  
 305 CCCAAGGCCCTCATCTTTGTGTCCATGAGCCGAGAGCAGTGGCGCGTATGAAGAG 364  
 Qy 361 CTGGCTGGATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACAGACCATGTTGGCCAC 420  
 Db |||||  
 365 CTGGCTGGATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACAGACCATGTTGGCCAC 424  
 Qy 421 GGACAGAGCAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTTCAGGAGTGTG 480  
 Db |||||  
 425 GGACAGAGCAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTTCAGGAGTGTG 484  
 Qy 481 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCCTTCTGGGC 540  
 Db |||||  
 485 TTGCAGCATGTGGATTCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCCTTCTGGGC 544  
 Qy 541 CACTCCATGGAGGGCCATCGCATCTCTACGGCGGAGAGAGCGCGGCCACTTCGCC 600  
 Db |||||  
 545 CACTCCATGGAGGGCCATCGCATCTCTACGGCGGAGAGAGCGCGGCCACTTCGCC 604  
 Qy 601 GGCATGTPACTCATTTGCGCTCTGTTCTTCGCAATCTGCAATCTGCAACAACTTCAAG 660  
 Db |||||  
 605 GGCATGTPACTCATTTGCGCTCTGTTCTTCGCAATCTGCAATCTGCAACAACTTCAAG 664  
 Qy 661 GTCCTTGTGCGAAAGTGTCTCAACTTGTGTGCGCAAACTTGTCCCTCGGGCCCATCGAC 720  
 Db |||||  
 665 GTCCTTGTGCGAAAGTGTCTCAACTTGTGTGCGCAAACTTGTCCCTCGGGCCCATCGAC 724  
 Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTTCGACATTTTAACTCAGACCCCTGATC 780  
 Db |||||  
 725 TCCAGCGTGTCTCTCGGAATAAGACAGAGTTCGACATTTTAACTCAGACCCCTGATC 784  
 Qy 781 TGCCGGGCGAGGCTG-AGGTGTGCTTCGGGATCCAACTGCTGAATGCC 828  
 Db |||||  
 785 TGCCGGGCGAGGCTGAAAGGTGTGCTTCGGGATCCAACTGCTGAATGCC 833

## RESULT 11

CN643629  
 LOCUS ILLUMIGEN MQO\_8210 Katze MMR Macaca mulatta cDNA clone IBIUW:3354

DEFINITION 5' similar to Bases 1 to 814 highly similar to human MGLL  
 (Hs.409826), mRNA sequence.

## ACCESSION

VERSION CN643629

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 815)

AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magnus

ILLUMIGEN Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagnus@illumigen.com

Sequenced on 2004.01.05. 794 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAAA

BACKWARD: CACTATAGGCGGATTTGGTA

Insert Length: 815 Std Error: 0.00

Plate: C1000097 row: C column: 03

Seq primer: CCCTCACTAAAGGGAACAAAA

POLYA=Yes.

FEATURES

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/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

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/clone\_lib="Katze MMR"

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Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis

kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold

Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 66.1%; Score 788.4; DB 7; Length 815;

Best Local Similarity 98.0%; Pred. No. 1.4e-202;

Matches 798; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 436 GAGAGGATGTAGTGTCTGACTTCCAGTTTTCGTACGGATGTGTTCAGCATGTGGAT 495

Db 61 GAGAGGATGTAGTGTCTGACTTCCAGTTTTCGTACAGATGTGTTCAGCATGTGGAT 120

Qy 496 TCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCCTTGGGCCACTCCATGGGAGGC 555

Db 121 TCCATGCAGAAAGACTACCTTGGGCTTCCTGCTTCCTTCTGGGCCACTCCATGGGAGGC 180

Qy 556 GCCATGCCATCTTCACGGCGCAGAGAGCGCGGCCACTTTCGCCGCGATGGTACTCAT 615

Db 181 GCCATGCCATCTTCACGGCGCAGAGAGCGCGGCCACTTTCGCCGCGATGGTACTCAT 240

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QY 976 GGTGCTACCATGTTCTCCAAAGAGCTTCTGAAAGTCAACAACTCGTCTTCCATGAA 1035
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QY 1036 ATAACATGTGGGTCTCTCAAGACAGCCAGGACAGGAACTGCTCCCAACCTGATG 1095
Db 661 ATAACATGTGGGTCTCTCAAGACAGCCAGGACAGGAACTGCTCCCAACCTGATG 720
QY 1096 CATTTGGCGGTGCGCGGCTCATGTCTGCGGGATGTCAGGAGGGGAGGAGATGGC 1155
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QY 1156 TTCTCAGATGCGTTCGCAAAAAA 1189
Db 781 TTCTCAGATGCGTTCGCAAAAAA 814
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RESULT 12
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LOCUS BQ686359 878 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8064425 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206212
5', mRNA sequence.
ACCESSION BQ686359
VERSION BQ686359.1 GI:21811675
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
National Library of Medicine
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2360 row: f column: 05
High quality sequence stop: 667.
Location/Qualifiers
1..878
/organism="Homo sapiens"
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/db_xref="caxon:9606"
/clone="IMAGE:6206212"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
FEATURES
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/clone lib="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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ORIGIN
Query Match 65.7%; Score 783.4; DB 5; Length 878;
Best Local Similarity 99.0%; Pred. No. 3.3e-201;
Matches 798; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
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Db 72 CCGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCCAGCGGACCCCGAGA 131
QY 218 GCATTCCCTACGAGGACCTCCCTCACCTGCTCAATGCAGACGACAGTACTCTTCTGCA 277
Db 132 GCATTCCCTACGAGGACCTCCCTCACCTGCTCAATGCAGACGACAGTACTCTTCTGCA 191
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Db 192 GGTACTGGAACCCACAGGACACCCAAAGGCCCTCATCTTTGTGCCATGGAGCCGAG 251
QY 338 AGCACAGTGGCGGTATGAAGAGCTGGCTCGATGCTGATGGGGCTGGACCTGCTGGTGT 397
Db 252 AGCACAGTGGCGGTATGAAGAGCTGGCTCGATGCTGATGGGGCTGGACCTGCTGGTGT 311
QY 398 TCGCCACAGACCATGTTGGCCAGGACAGAGCGAGGAGGAGGATGCTAGTGTCTGACT 457
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QY 458 TCCACGTTTTTCGTGAGGGATGTTGTCAGCATGTGGATTCATGCAGAAAGACTACCCGT 517
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QY 518 GGCTTCCTGCTTCTTCCTTCTGGGCACATCCATGGAGGGCCATCGCATCTCAGGCGG 577
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QY 578 CAGAGAGCGCGGCGCATCTCGCGCATGTACTCATTTTCGCCCTCTGTTCTTCCCAATC 637
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QY 638 CTGAATCTGCAACAACTTCAAGGTCTTGTGCGAAAGTCTCAACCTTGTGTGCGCAA 697
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QY 698 ACTTGTCCCTCGGGCCCATGACTCCAGCGTCTCTCGGAATAAGACAGAGTTCGACA 757
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Db 852 TAGCAAGAGCCCGAGGACAGACTCT 877
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BUI45364      916 bp      mRNA      linear      EST 03-SEP-2002
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ACCESSION      BUI45364
VERSION      BUI45364.1 GI:22658896
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 916)
              NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: DCTD/DFP
              cDNA Library Preparation: Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LUCM2332 row: j column: 08
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              /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; CDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGCACGAG(G). Library constructed by Ling Hong in the
              laboratory of Gerald M. Rubin (University of California,
              Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
              Superscript II RT (Life Technologies). Note: this is a
              NIH_MGC Library."
ORIGIN
Query Match      64.8%; Score 772.2; DB 5; Length 916;
Best Local Similarity 96.8%; Pred. No. 3.7e-198;
Matches 798; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 158 CAGGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCGCGGACCCCGCAGA 217
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DB 77 CCGACCTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCCGCGGACCCCGCAGA 136
QY 218 GCATTCCCTACAGGACCTCCCTCACCTGGTCAATGACGACGACGACGACGACGAC 277
DB |
DB 137 GCATTCCCTACAGGACCTCCCTCACCTGGTCAATGACGACGACGACGACGACGAC 196
QY 278 GGTACTGGAACCCACAGGACACCCAGAGCCCTCATCTTTGTGTCCATGGAGCCGAG 337
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DB 197 GGTACTGGAACCCACAGGACACCCAGAGCCCTCATCTTTGTGTCCATGGAGCCGAG 256
QY 338 AGCAGGTGGCCGTATGAAGAGTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGT 397
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DB 257 AGCAGGTGGCCGTATGAAGAGTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGT 316
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DB 317 TCGCCCAAGACCATGTTGGCCACGACACGACAGCGAAGGGGAGAGGATGTTAGTGTGACT 376
QY 458 TCCAGGTTTTGTCAGGAGATGTTGACAGCATGTGGATTCATGACAGAAAGACTACCTGT 517
DB |
DB 377 TCCAGGTTTTGTCAGGAGATGTTGACAGCATGTGGATTCATGACAGAAAGACTACCTGT 436

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QY 518 GGCTTCCTGTCTTCTTCTGGGCATCTCCATGGAGGCGGCATCGCCATCTCTACGGCG 577
DB |
DB 437 GGCTTCCTGTCTTCTTCTGGGCATCTCCATGGAGGCGGCATCGCCATCTCTACGGCG 496
QY 578 CAGAGAGGCGGGCCACTTCCCGGCGATGCTACTCATTTGCGCTTCTGTTCTTGGCAATC 637
DB |
DB 497 CAGAGAGGCGGGCCAGTTCCCGGCGATGCTACTCATTTGCGCTTCTGTTCTTGGCAATC 556
QY 638 CTGAATCTGCAACAACATTTCAAGGTCTTGTGCGAAAGTGTCTCAACTTGTGTGTCGCAA 697
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DB 557 CTGAATCTGCAACAACATTTCAAGGTCTTGTGCGAAAGTGTCTCAACTTGTGTGTCGCAA 616
QY 698 ACTTGTCCCTCGGCGCCATCGATCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCGACA 757
DB |
DB 617 ACTTGTCCCTCGGCGCCATCGATCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCGACA 676
QY 758 TTTATAACTCAGACCCCTCATCTGCGGCGACGGCTGAAGGTGTGCTTCGGCATCCAAC 817
DB |
DB 677 TTTATAACTCAGACCCCTCATCTGCGGCGACGGCTGAAGGTGTGCTTCGGCATCCAAC 736
QY 818 TGCTGAATGCGTCTCACGGGTGGAGCGCCCTTCCCAAGCTGACTGTGCTTCTCTGTC 877
DB |
DB 737 TGCTGAATGCGTCTCACGGGTGGAGCGCCCTCGCAAGCTGACTTGGGCGCTTCTGTC 796
QY 878 TGCTCCAGGCTCTGCGCATCGCTATGTGACAGCAAGGGGCTACTGCTCATGGAGT 937
DB |
DB 797 TGCTCCAGGCTCTGCGCATCGCTGTGACAGCAAGGGGCTACTGCTCCGGGAGG 856
QY 938 TAGCC--AAGAGCCAGGACCAAGACTCTCAAGATTATGAAGGTG 979
DB |
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LOCUS      603023793F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:519462 5',
DEFINITION      mRNA sequence.
ACCESSION      BUI58109
VERSION      BUI58109.1 GI:15749687
KEYWORDS      EST.
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ORGANISM      Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 806)
              NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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              /clone_lib="NIH_MGC_114"
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              Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
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              upon cloning). Average insert size 1.5 kb, insert size

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range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

ORIGIN		Query Match	64.5%;	Score 768.8;	DB 4;	Length 806;
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QY	282	CTGAAACCCACAGCACACCAAGGCCCTCATCTTTGTGCCATGGAGCGGAGACA	341			
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QY	342	CAGTGGCCCTATGAGAGCTGGCTCGCATCTGATGGGGTGGACCTGTGGTTCGC	401			
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QY	402	CCACGACCATGTGGCCACGACAGACGCGAAGGGGAGAGGATGGTAGTCTGACTTCCA	461			
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QY	522	TCCTGTCTCTTCTGGGCCACTCCATGGAGGGGCCATCGCCATCTCAGGGCGGAGA	581			
Db	241	TCCTGTCTCTTCTGGGCCACTCCATGGAGGGGCCATCGCCATCTCAGGGCGGAGA	300			
QY	582	GAGCGGGGCGACATCGCGGCATGGTACTCATTTTCGCTCTGTGTTTGCATCTCTGA	641			
Db	301	GAGCGGGGCGACATCGCGGCATGGTACTCATTTTCGCTCTGTGTTTGCATCTCTGA	360			
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QY	702	GTCCCTCGGGCCATCGACTCGAGGTGCTCTCTCGGAATAAGACAGAGTTCGACATTTA	761			
Db	421	GTCCCTCGGGCCATCGACTCGAGGTGCTCTCTCGGAATAAGACAGAGTTCGACATTTA	480			
QY	762	TAACTCAGACCCCTGTATCTCGGGGAGGGCTGAAGTGTGCTTCGGCATCCCAACTGCT	821			
Db	481	TAACTCAGACCCCTGTATCTCGGGGAGGGCTGAAGTGTGCTTCGGCATCCCAACTGCT	540			
QY	822	GAATGCCGTCTCAGGGTGGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTGCTGCT	881			
Db	541	GAATGCCGTCTCAGGGTGGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTGCTGCT	600			
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QY	942	CAAGAGCCAGACAGACTCTCAAGATTATGAAGTGGCC-TACCATGTTCTCCACACAGG	1000			
Db	660	CAAGAGCCAGACAGACTCTCAAGATTATGAAGTGGCC-TACCATGTTCTCCACACAGG	719			
QY	1001	AGCTTCTCGAAGTACCACAACTCCGTCCTTCCATGAATAAATGTGGGTCTCTCAAGGA	1060			
Db	720	AGCTTCTCGAAGTACCACAACTCCGTCCTTCCATGAATAAATGTGGGTCTCTCAAGGA	778			
QY	1061	CAGCCACGGCAGGAACCTCGTCCCCACC	1088			
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RESULT 15  
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LOCUS  
DEFINITION BUI69041 885 bp mRNA linear EST 04-SEP-2002  
5', mRNA sequence.  
AGENCOURT 7974194 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082332  
ACCESSION BUI69041

BUI69041.1 GI:22683025  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
1 (bases 1 to 885)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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ORIGIN		Query Match	64.2%;	Score 765.8;	DB 5;	Length 885;
		Best Local Similarity	98.0%;	Pred. No. 2e-196;		
		Matches 797;	Conservative 0;	Mismatches 12;	Indels 4;	Gaps 2;
QY	158	CAGACCTTGAAGACCTTCCAGCATGCCAGAGAAAGTTCCTCCAGGGGACCCCGAGA	217			
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QY	218	GCATTCCTTACCCAGACCTCCCTCACCTGGTCAATGCAGCGGACAGTACCTCTTCTGCA	277			
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Db	252	AGCACAGTGGCGCTATGAAGAGCTGGCTGGATGCTGATGGGGCTGGACCTGCTGTGT	311			
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Db	312	TCGCCCCACGACCATGTGTGGCCACGACAGCGAAGGGGAGAGGATGCTAGTGTCTGACT	371			
QY	458	TCCACGTTTTCGTCAGGGATGTGTGCGCATGTGGATTCCATCAGAAAGACTACCCCTG	517			
Db	372	TCCACGTTTTCGTCAGGGATGTGTGCGCATGTGGATTCCATCAGAAAGACTACCCCTG	431			
QY	518	GGCTTCCTGTCTTCTTCTGGCCACTCCATGGAGGGCCCATGCCATCTCTCAGGCCG	577			
Db	432	GGCTTCCTGTCTTCTTCTGGCCACTCCATGGAGGGCCCATGCCATCTCTCAGGCCG	491			
QY	578	CAGAGAGCGGGCGACCTTCGCGGGCATGGTACTCAITTCGCCCTCTGTGTTCTTGCCAATC	637			



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1192	100.0	1192	6	AX410763	AX410763 Sequence
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4	1192	100.0	1192	9	HSU67963	U67963 Human lysop
5	1192	100.0	1573	9	BC006230	BC006230 Homo sapi
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7	1169.8	98.1	1890	9	AK091314	AK091314 Homo sapi
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12	702	58.9	1316	10	BC057965	BC057965 Mus muscu
13	701.8	58.9	3600	10	MMU001118	AJ001118 Mus muscu
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19	378.4	31.7	1972	5	BC082452	BC082452 Xenopus l

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	21	363.4	30.5	517	6	AR415884	AR415884 Sequence
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ALIGNMENTS

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LOCUS CQ861598 1192 bp DNA linear PAT 10-SEP-2004  
DEFINITION Sequence 231 from Patent WO2004072465.  
ACCESSION CQ861598  
VERSION CQ861598.1 GI:51982587  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Burczynski, M., Twine, N., Dörner, A. J. and Trepicchio, W. L.  
TITLE METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO / I  
JOURNAL Patent: WO 2004072265-A 231 26-AUG-2004:  
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);  
Dörner, Andrew J. (US); Trepicchio, William L. (US)  
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DEFINITION Sequence 3410 from Patent WO0229103.  
ACCESSION AX410763  
VERSION AX410763.1 GI:21443468

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.  
TITLE Gene expression profiles in liver cancer  
JOURNAL Patent: WO 0229103-A 3410 11-APR-2002;  
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    Best Local Similarity 100.0%; Pred. No. 7e-276;  
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DEFINITION Human lysophospholipase homolog (HU-K5) mRNA, complete cds.
VERSION U67963
SOURCE U67963.1 GI:1763010
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1192)
AUTHORS Upton,C. and Buller,R.M.L.
TITLE Human homolog of an ectromelia virus protein has similarity to
E.coli lysophospholipase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1192)
AUTHORS Upton,C. and Buller,R.M.L.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-1996) Biochemistry and Microbiology, University
of Victoria, 150 Petch Building, Victoria, BC V8W 2Y2, Canada
REFERENCE 3 (bases 1 to 1192)
AUTHORS Wall,E.M., Cao,J., Chen,N., Buller,R.M. and Upton,C.
TITLE A novel poxvirus gene and its human homolog are similar to an E.
coli lysophospholipase
JOURNAL Virus Res. 52 (2), 157-167 (1997)
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PUBMED 9495531
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ACCESSION BC006230
VERSION BC006230.2 GI:38197481
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SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Hominiidae; Homo.

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REFERENCE 1 (bases 1 to 1573)  
 AUTHORS Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J. and Marra M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1573)  
 AUTHORS Strausberg R.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT On Nov 6, 2003 this sequence version replaced gi:13623260.  
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 Email: [gcaps@remail.nih.gov](mailto:gcaps@remail.nih.gov)  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Sequencing Center (NISC), Gaithersburg, Maryland  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
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	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
JOURNAL	12477932		
PUBMED	2 (bases 1 to 1192)		
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AUTHORS	Direct Submission		
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JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
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DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@nhgri.nih.gov">nisc_mgc@nhgri.nih.gov</a> Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.			
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Qy	1142	AGGCGAGAGATGGCTTCTCAGATATGGCTGTCAGAAAAAATTTTTTTTTTTT	1192	
Db	1141	AGGCGAGAGATGGCTTCTCAGATATGGCTGTCAGAAAAAATTTTTTTTTTTT	1191	
RESULT 7				
LOCUS	AK091314	1890 bp	mRNA	linear
DEFINITION	Homo sapiens cDNA FLJ33995 fis, clone DFNES2008160, highly similar to Human lysophospholipase homolog (HU-K5) mRNA.			
ACCESSION	AK091314			
VERSION	AK091314.1	GI:21749655		
KEYWORDS	oligo capping; fis (full insert sequence).			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1			

## AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Oteuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Iehii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nishitani, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hoshiro, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Tanikawa, K., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Hirakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuka, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A., Hara, H., Tanabe, T., Nomura, Y., Togiyama, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mueshino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terauchi, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Takahashi, T., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.

## TITLE

Complete sequencing and characterization of 21,243 full-length human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

## JOURNAL

14702039

## PUBMED

REFERENCE

## AUTHORS

2

Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Oteuki, T., Sato, H., Wakamatsu, A., Iehii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.

## Unpublished

NEDO human cDNA sequencing project

## 3 (bases 1 to 1890)

Isogai, T. and Yamamoto, J.

## Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

## COMMENT

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

## Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DFNES2008160"

/cell\_type="normal dermal fibroblasts (Neonatal Skin) (NHDF2564)"

/note="cloning vector: pME18SFL3-primary culture, normal dermal fibroblasts"

## ORIGIN

Query Match 98.1%; Score 1169.8; DB 9; Length 1890; Best Local Similarity 99.8%; Pred. No. 1.5e-270;



Matches 1171; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1	CCAGCCGAAAGG	CAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGTGCCTTCCTCTGTGCC	60					
Db	718	CCAGCCGAAAGG	CAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGTGCCTTCCTCTGTGCC	777					
Qy	61	TTGGGGCCGCG	CAGATGAGGAAACAGCCGATTTGCCCTGGTTCTGATTTCTCCAGGCTGTC	120					
Db	778	TTGGGGCCGCG	CAGATGAGGAAACAGCCGATTTGCCCTGGTTCTGATTTCTCCAGGCTGTC	837					
Qy	121	GTGGTTGTG	GAATGCAACGCGCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC	180					
Db	838	GTGGTTGTG	GAATGCAACGCGCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC	897					
Qy	181	ATGCCAGAG	AAAGTTCCCCCAGAGCGGACCCCGCAGAGCATTCCTTACGAGCACTCCCT	240					
Db	898	ATGCCAGAG	AAAGTTCCCCCAGAGCGGACCCCGCAGAGCATTCCTTACGAGCACTCCCT	957					
Qy	241	CACCTGGT	CAATGCAGCGGACAGTACCTCTCTGCAGGTACTGGAACCCACAGGCACA	300					
Db	958	CACCTGGT	CAATGCAGCGGACAGTACCTCTCTGCAGGTACTGGAACCCACAGGCACA	1017					
Qy	301	CCCAAGGC	CCCTCATCTTTGTGTCCCATGGAGCGGAGACACAGTGGCGCTATGAAGAG	360					
Db	1018	CCCAAGGC	CCCTCATCTTTGTGTCCCATGGAGCGGAGACACAGTGGCGCTATGAAGAG	1077					
Qy	361	CTGGCTCG	ATGATGGGCTGGACCTGTGTGTTCGCCACGACCATGTTGGGCAC	420					
Db	1078	CTGGCTCG	ATGATGGGCTGGACCTGTGTGTTCGCCACGACCATGTTGGGCAC	1137					
Qy	421	GGACAG	CGAAGGGGAGAGATGGTAGTGTCTGACCTTCCAGTTTCGTGAGGATGTG	480					
Db	1138	GGACAG	CGAAGGGGAGAGATGGTAGTGTCTGACCTTCCAGTTTCGTGAGGATGTG	1197					
Qy	481	TTGACG	CATGTGGAATTCATGCAGAAAGACTACCTGGGCTTCCTGTCTTCCTCTGGGC	540					
Db	1198	TTGACG	CATGTGGAATTCATGCAGAAAGACTACCTGGGCTTCCTGTCTTCCTCTGGGC	1257					
Qy	541	CACTCC	ATGGAGGCGCCATCGCCATCTCAGGCGCAGAGAGGCGGGCCTTGCC	600					
Db	1258	CACTCC	ATGGAGGCGCCATCGCCATCTCAGGCGCAGAGAGGCGGGCCTTGCC	1317					
Qy	601	GGCATGG	TACTCATTTGCCCTCTGTCTTCCCAATCTGGAATCTGCAACAACCTTTCAAG	660					
Db	1318	GGCATGG	TACTCATTTGCCCTCTGTCTTCCCAATCTGGAATCTGCAACAACCTTTCAAG	1377					
Qy	661	GTCTTGT	CTGCGAAAGTCTCAACCTTGTGTGTCAAACTTTGTCCCTCGGGCCCATCGAC	720					
Db	1378	GTCTTGT	CTGCGAAAGTCTCAACCTTGTGTGTCAAACTTTGTCCCTCGGGCCCATCGAC	1437					
Qy	721	TCCAGCG	TGCTCTCGGAATTAAGACAGAGTGCACATTTATTAACTCAGACCCCTGATC	780					
Db	1438	TCCAGCG	TGCTCTCGGAATTAAGACAGAGTGCACATTTATTAACTCAGACCCCTGATC	1497					
Qy	781	TGCCGG	CAGGCGTGTAAGTGTCTCGGCATCCAACTGCTGAATCCCGTCTCAGCGGTG	840					
Db	1498	TGCCGG	CAGGCGTGTAAGTGTCTCGGCATCCAACTGCTGAATCCCGTCTCAGCGGTG	1557					
Qy	841	GAGCGC	CCCTCCCCCAAGCTGACTGTGCCCCCTTCTGTGCTCCAGGGCTCGCCGATCGC	900					
Db	1558	GAGCGC	CCCTCCCCCAAGCTGACTGTGCCCCCTTCTGTGCTCCAGGGCTCGCCGATCGC	1617					
Qy	901	CTATGT	GCAGCAAAAGGGGCTTACTGTCTATGAGTTTAGCCAGAGCCAGGACAAGACT	960					
Db	1618	CTATGT	GCAGCAAAAGGGGCTTACTGTCTATGAGTTTAGCCAGAGCCAGGACAAGACT	1677					
Qy	961	CTCAAG	ATTTTATGAGGTGCCTACCATGTTCTCCACAGGAGCTTCTCTGAAGTCAACAC	1020					
Db	1678	CTCAAG	ATTTTATGAGGTGCCTACCATGTTCTCCACAGGAGCTTCTCTGAAGTCAACAC	1737					
Qy	1021	TCCGTCT	TTCCATGAAATAAATGTGGTCTCTCAAGGACAGCCACGGCAGGAATGCG	1080					
Db	1738	TCCGTCT	TTCCATGAAATAAATGTGGTCTCTCAAGGACAGCCACGGCAGGAATGCG	1797					

Qy	1081	TCCCCACCCTGA	TGCAATTCGCGGTGCCCGGTCTCATGGTCTGGGGATGCAGCAGGGG	1140					
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Qy	1141	AAGGGCAG	AGATGGCTTCTCAGATATGGCTTGC	1173					
Db	1858	AAGGGCAG	AGATGGCTTCTCAGATATGGCTTGC	1890					
RESULT 8									
AX281732									
LOCUS	AX281732		4193 bp	DNA	linear	PAT 02-NOV-2001			
DEFINITION	Sequence 141 from Patent WO01/77389.								
ACCESSION	AX281732								
VERSION	AX281732.1		GI:16608983						
KEYWORDS									
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	1								
AUTHORS	Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J., Mikita,T. and Tai,J.								
TITLE	Genes expressed in foam cell differentiation								
JOURNAL	Patent: WO 0177389-A 141 18-OCT-2001;								
FEATURES	Incyte Genomics, Inc. (US)								
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	/organism="Homo sapiens"								
	/mol_type="unassigned DNA"								
	/db_xref="taxon:9606"								
	/note="Incyte ID No: 216063.17"								
ORIGIN									
Query Match		97.5%;	Score 1162;	DB 6;	Length 4193;				
Best Local Similarity		99.9%;	Pred. No. 1.1e-268;						
Matches 1173; Conservative		0;	Mismatches 0;	Indels 1;	Gaps 1;				
Qy	1	CCAGCCGAAAGG	CAGGGTCTGGGTGCGGAAAGAGGCTCGGAGCTGCCCTTCCTGTGTGCC	60					
Db	452	CCAGCCGAAAGG	CAGGGTCTGGGTGCGGAAAGAGGCTCGGAGCTGCCCTTCCTGTGTGCC	511					
Qy	61	TTGGGGCGCC	CAGATCAGGGAACAGCCCGATTTGCCCTGTTCTGATTCTCCAGGCTGTC	120					
Db	512	TTGGGGCGCC	CAGATCAGGGAACAGCCCGATTTGCCCTGTTCTGATTCTCCAGGCTGTC	571					
Qy	121	GTGTTTGTG	GAATGCAAAACGCCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC	180					
Db	572	GTGTTTGTG	GAATGCAAAACGCCAGCACATAATGGAACAGGACCTGAAGACCTTCCAGC	631					
Qy	181	ATGCCAGAG	AAAGTTCCCCCAGCGGACCCCGCAGAGCATTCCTTACGAGGACCTCCCT	240					
Db	632	ATGCCAGAG	AAAGTTCCCCCAGCGGACCCCGCAGAGCATTCCTTACGAGGACCTCCCT	691					
Qy	241	CACCTGCT	CAATGCAGCGGACAGTACTCTTCTGCGAGGTACT-GGAAACCCACAGGCAC	299					
Db	692	CACCTGCT	CAATGCAGCGGACAGTACTCTTCTGCGAGGTACTGGAAACCCACAGGCAC	751					
Qy	300	ACCCAAG	CCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGA	359					
Db	752	ACCCAAG	CCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCCGCTATGAAGA	811					
Qy	360	GCTGGCT	CGAATGTGATGGGGCTGGACCTGTGCTGGTGTTCGCCACGACCATGTTGGCCA	419					
Db	812	GCTGGCT	CGAATGTGATGGGGCTGGACCTGTGCTGGTGTTCGCCACGACCATGTTGGCCA	871					
Qy	420	CGGACAG	CGAAGGGGAGAGGATGGTAGTCTGACTTCCACGTTTTCGTTCAGGATGT	479					
Db	872	CGGACAG	CGAAGGGGAGAGGATGGTAGTCTGACTTCCACGTTTTCGTTCAGGATGT	931					
Qy	480	GTTGCAG	CATGTGGATTTCCATGCAGAAAGACTACCTCGGGCTTCCTGTCTTCTCTGGG	539					





Db	301																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												</
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```

Db      661 GAGCGCGCCCTCCCAAGCTGACTGTGCGCCTTCCTGCTGCCAGGGCTCTGCCGATCGC 720
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Qy      961 CTCAGAGTTTATGAAGGTGCTTACCATTGCTTCTCCCAAGAGCTTCTTGAAGTCAACCAAC 1020
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Qy      1021 TCCGCTCTCCATGAATAAATGATGGTCTCTCTCAAGAGCAGCCACCGCAGGAAGTGGC 1080
Db      841 TCCGCTCTCCATGAATAAATGATGGTCTCTCAAGAGCAGCCACCGCAGGAAGTGGC 900
Qy      1081 TCCCCACCCCTGA 1092
Db      901 TCCCCACCCCTGA 912

RESULT 11
LOCUS   MMU316580          3863 bp      mRNA      linear      ROD 12-SEP-2001
DEFINITION Mus musculus mRNA for monoglyceride lipase (Mgll gene), transcript
2.
ACCESSION AJ316580
VERSION   AJ316580.1  GI:15617371
KEYWORDS alternative splicing; Mgll gene; monoglyceride lipase.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS   Karlsson,M., Contreras,J.A., Hellman,U., Tornqvist,H. and Holm,C.
TITLE     cDNA cloning, tissue distribution, and identification of the
catalytic triad of monoglyceride lipase. Evolutionary relationship
to esterases, lysophospholipases, and haloperoxidases
J. Biol. Chem. 272 (43), 27218-27223 (1997)
98001701
PUBMED   9341166
REFERENCE 2
AUTHORS   Karlsson,M., Reue,K., Xia,Y.R., Lusis,A.J., Langin,D., Tornqvist,H.
and Holm,C.
TITLE     Exon-intron organization and chromosomal localization of the mouse
monoglyceride lipase gene
Gene 272 (1-2), 11-18 (2001)
JOURNAL  21363420
PUBMED   11470505
REFERENCE 3
AUTHORS   Holm,C.
TITLE     Direct Submission
Submitted (15-AUG-1997) Holm C., Cell and Molecular Biology, Lund
University, P.O. Box 94, S-221 00 Lund, SWEDEN
Revised by [4]
JOURNAL  4 (bases 1 to 3863)
REFERENCE 4
AUTHORS   Holm,C.
TITLE     Direct Submission
Submitted (12-SEP-2001) Holm C., Cell and Molecular Biology, Lund
University, P.O. Box 94, S-221 00 Lund, SWEDEN
Related sequence: AJ001118. (alternative 5'UTR).
Location/Qualifiers
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mRNA
5' UTR

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3844..3849
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/citation=[2]

3'UTR

polyA_signal

ORIGIN

Query Match      63.4%; Score 756.2; DB 10; Length 3863;
Best Local Similarity 81.7%; Pred. No. 4.8e-171;
Matches 922; Conservative 0; Mismatches 203; Indels 4; Gaps 4;

Qy 31 AAGAGGGCTCGAGACTGCTTCCTGCTGCTGGGGCGCCAGATGAGGGAACAGCCGG 90
Db 222 AGCGGGGAGGCGCGGACCCCGTGTGCTGCTGCGCGCGCGATGAGGGAACAGCCGG 281
Qy 91 -ATTGCTGCTGCTTCGATTCCTCAGGCTGCTGCTGCGAAATGCAACGCCAGACAT 149
Db 282 GCTTGGCTGCGCTGATCTCGAGGCTGCGCGGTAGTGGAAATGCAACGCCAGAC-T 340
Qy 150 AATGGAACAGGACCTCTGAAGACCTCTCCAGCATGCCAGAGGAAAGTTCCCCAGCGGAC 209
Db 341 AATGGAACAGGCGCTTAAAGACCCCTGCAGGATGCTGAGGCAAGTTCAACCGCGAAC 400
Qy 210 CCCGAGAGCATTCCTTACAGGACCTCCCTCAGCTGCTCAATGCAGAGGACAGTACT 269
Db 401 TCCACAGAAATTCCTTACAGGACCTGCTCCTCAGCTGCTCAATGCAGAGGACAGTACT 460
Qy 270 CTCTGAGGTACTGGAAACCCACAGGACACCCAGGCGCTCATCTTTGTGCCATGG 329
Db 461 CTTTGTAGATACTGGAAAGCCCTGCGCACACCCAGGCGCTCATCTTTGTGCCATGG 520
Qy 330 AGCGGAGAGCACAGTGGCGCTATGAAGAGCTGGCTCGGATGCTGATGGGGCTGGACCT 389
Db 521 AGCTGGGGAACACATGTGGCGCTTATGATGAGCTGGCTCATATGTAAGGGGCTGGACAT 580
Qy 390 GCTGGTGTGCGCCACAGCATGTTGGCCACGAGCAGAGCGAAGGGAGAGAGATGTTAGT 449
Db 581 GCTGGTATTTGCCCATGACCATGTTGGCCATGGGCGAGAGTGGGAGAGAGATGTTGTT 640
Qy 450 GTCTGACTTCCACCTTTTCTGTCAGGATGCTGTCAGCATGTGGATTCATGCGCAAGA 509
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Matches 827; Conservative 0; Mismatches 172; Indels 2; Gaps 2;
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ACCESSION AY081195
VERSION AY081195.1 GI:19697885
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 912)
AUTHORS Dinh,T.P., Carpenter,D., Leslie,F.M., Freund,T.F., Katona,I.,
Sensi,S.L., Kathuria,S. and Piomelli,D.
TITLE Brain monoglyceride lipase participating in endocannabinoid
inactivation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (16), 10819-10824 (2002)
PUBMED 12136125
REFERENCE 2 (bases 1 to 912)
AUTHORS Dinh,T.P. and Piomelli,D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Pharmacology, UC Irvine, 360 Med Surge II,
Irvine, CA 92697, USA
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## ORIGIN

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QY 481 TTGCAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTCTCTCTGGGC 540
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RESULT 15
LOCUS CO729628 667 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15562 from Patent WO02068579.
ACCESSION CO729628
VERSION CO729628.1 GI:42301233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15562 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 99.8%; Pred. No. 3.9e-131;
Matches 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GACCTGAAGACCCCTTCCAGCATGCCAGAGAAAGTTCCCGGAGGCGGACCCCGCAGAGCA 60
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Job time : 5204 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 23:49:38 ; Search time 669 Seconds  
(without alignments)  
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Title: U67963

Perfect score: 1192

Sequence: 1 CCAGCCGAAAGGCGGGTC.....CAAAAAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2: Geneseqn1990s.\*  
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13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1192	100.0	1192	13 ADS2880	ADS2880 Drug ther
6	1192	100.0	1582	13 ADP14672	ADP14672 Human NF-
7	1192	100.0	1582	13 ADP24423	ADP24423 PRO polyp
8	1191	99.9	1192	12 ADO39191	ADO39191 Human cDN
9	1167	97.9	1192	12 ADL56807	ADL56807 Human SEC
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11	1096	91.9	1613	10 ADI21843	ADI21843 Novel hum
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19	609	51.1	791	12 ADL57003	ADL57003 SECX-rela
20	519.8	43.6	556	9 ACH42006	ACH42006 Human foe

21	464.4	39.0	576	5 AAS90608	Aas90608 DNA encod
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25	364.8	30.6	425	9 ACH20621	Ach20621 Human adu
26	355.2	29.8	393	2 AAQ61398	Aaq61398 Human bra
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37	116.2	9.7	110000	4 AAI99682_02	Continuation (3 of
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ALIGNMENTS

RESULT 1  
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ID ABL59515 standard; cDNA; 1192 BP.

AC ABL59515;

XX 16-JUL-2002 (first entry)

XX Human lysophospholipase homologue cDNA SEQ ID NO:15.

DE Human; lysophospholipase homologue; enzyme; tumour;

KW Human; lysophospholipase homologue; enzyme; tumour;

KW Lipid associated gene; lipid metabolism; lipid synthesis; gene; se.

XX Homo sapiens.

XX WO200227028-A1.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-US030366.

XX 28-SEP-2000; 2000US-00676052.

XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.

XX Skinner MK, Patton JL, Chaudhary J;

XX WPI; 2002-405056/43.

XX Identifying tumor characteristics in a tissue sample taken from a patient, involves determining the copy number or expression level of genes associated with lipid metabolism, synthesis or action.

XX Example 1; Page 74; 113pp; English.

XX The present invention describes a method for identifying tumour characteristics, comprising measuring a copy number or expression level of at least two genes associated with lipid metabolism, synthesis, or action in cells from a patient tissue sample, and comparing the results with a copy number or expression level of the genes in a normal cell. Also described is an array of nucleic acid polymers immobilised on a solid support, comprising a solid support, at least two different nucleic acid polymers which are each specific for a different gene associated

CC with lipid metabolism, synthesis or action, where each nucleic acid  
CC polymer is located at a predetermined position on the solid support, and  
CC the array comprises nucleic acid polymers which are specific for less  
CC than 100 genes other than the selected genes. The method is useful for  
CC determining tumour characteristics in a tissue sample taken from a  
CC patient. The present sequence represents a human lipid-associated gene  
CC related cDNA sequence, which is used in the exemplification of the  
CC present invention  
XX

SEQ Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGACAGTGGCGGTATGAAGAG 360  
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DB 601 GGCATGTGACTCATTTGCGCTTGGTCTGCGAATCTGGAATCTGCAAGAACTTTCAAG 660  
QY 661 GTCCTTGTGCGAAAGTCTCAACTTGTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720  
DB 661 GTCCTTGTGCGAAAGTCTCAACTTGTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720  
QY 721 TCCAGCGGTCTCTTCGGAATAAGACAGAGTGCACATTTTATACTCAGACCCCTGATC 780  
DB 721 TCCAGCGGTCTCTTCGGAATAAGACAGAGTGCACATTTTATACTCAGACCCCTGATC 780  
QY 781 TCCCGGCGAGGCTGCAAGGTGCTTGGGCATCAACTGCTGATTCGGTCTCAGGGGTG 840  
DB 781 TCCCGGCGAGGCTGCAAGGTGCTTGGGCATCAACTGCTGATTCGGTCTCAGGGGTG 840  
QY 841 GAGCGCGCCCTCCCAAGCTGACTGTGCTTCTGCTGCTCCAGGGCTCTGCGGATCGC 900  
DB 841 GAGCGCGCCCTCCCAAGCTGACTGTGCTTCTGCTGCTCCAGGGCTCTGCGGATCGC 900

DB 841 GAGCGCGCCCTCCCAAGCTGACTGTGCTGCTCTCTGCTCTCCAGGCTCTGCCGATCGC 900  
QY 901 CTATGTGACAGCAAAAGGGGCTTACCTCTCATGAGTTAGCAAGAGCCAGCAAGACT 960  
DB 901 CTATGTGACAGCAAAAGGGGCTTACCTCTCATGAGTTAGCAAGAGCCAGCAAGACT 960  
QY 961 CTCGAAGTTTATGAAGGTGCTACCATGTTCTCCACAAGGAGCTTCTGAGTCAACCAAC 1020  
DB 961 CTCGAAGTTTATGAAGGTGCTACCATGTTCTCCACAAGGAGCTTCTGAGTCAACCAAC 1020  
QY 1021 TCCGCTTTCATGAATAAATCAATGTGGGTCTCTCAAAAGGACAGCCAGGAGGAAGTGGC 1080  
DB 1021 TCCGCTTTCATGAATAAATCAATGTGGGTCTCTCAAAAGGACAGCCAGGAGGAAGTGGC 1080  
QY 1081 TCCGCCACCTGAAATGCAATTTGGCGGTGCCGGCTCATGCTCTGCGGATGTCAGCAGGGG 1140  
DB 1081 TCCGCCACCTGAAATGCAATTTGGCGGTGCCGGCTCATGCTCTGCGGATGTCAGCAGGGG 1140  
QY 1141 AAGGGCAGAGATGCTTCTCAGATATGCTTGCATAAAAAAAGGAGGAGGAGGAGGAGG 1192  
DB 1141 AAGGGCAGAGATGCTTCTCAGATATGCTTGCATAAAAAAAGGAGGAGGAGGAGGAGG 1192

RESULT 2  
ABK84407  
ID ABK84407 standard; cDNA; 1192 BP.  
XX AC ABK84407;  
XX AC  
DT 14-AUG-2002 (first entry)  
XX  
DE Human cDNA differentially expressed in granulocytic cells #978.  
XX  
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX  
OS Homo sapiens.  
XX  
FN WO200228999-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US030821.  
XX  
PR 03-OCT-2000; 2000US-0237189P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX  
DR WPI; 2002-435328/46.  
XX

PT Detecting granulocyte activation by detecting differential expression of  
PT genes associated with granulocyte activation, which serves as diagnostic  
PT markers that is useful for monitoring disease states and drug toxicity.  
XX  
PS Claim 1; SEQ ID NO 978; 114pp; English.  
XX  
CC The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing the  
CC expression level to an expression level in an unactivated GC, where  
CC differential expression of Gs is indicative of GCA. Also included are  
CC modulating (M2) GA by contacting GC with an agent that alters the  
CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
CC capable of modulating GCA or an inflammation (especially chronic) in a  
CC tissue, an allergic response in a subject, exposure of a subject to a

pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue; an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 100.0%; Score 1192; DB 6; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCAGCCGAAAGGAGGCTCTGGTGGGAGAGGGCTGGAGCTGCCTTCCTGCTGCC	60
Db	1	CCAGCCGAAAGGAGGCTCTGGTGGGAGAGGGCTGGAGCTGCCTTCCTGCTGCC	60
Qy	61	TTGGGGCCGCCAGATGAGGAAACAGCCCGATTTGCTGTTCTGATTTCTCAGGCTGTC	120
Db	61	TTGGGGCCGCCAGATGAGGAAACAGCCCGATTTGCTGTTCTGATTTCTCAGGCTGTC	120
Qy	121	GTGGTTGTGGAATGCAACCGCAGACATATGAAACAGAGCCTGAAGACCTTCAGC	180
Db	121	GTGGTTGTGGAATGCAACCGCAGACATATGAAACAGAGCCTTCAGACCTTCAGC	180
Qy	181	ATGCCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT	240
Db	181	ATGCCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT	240
Qy	241	CACCTGTGTAATGACAGCGGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGCACA	300
Db	241	CACCTGTGTAATGACAGCGGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGCACA	300
Qy	301	CCCAAGGCCCTCATCTTTGTGTCATGAGCGGAGAGCAGTGGCGGCTATGAAGAG	360
Db	301	CCCAAGGCCCTCATCTTTGTGTCATGAGCGGAGAGCAGTGGCGGCTATGAAGAG	360
Qy	361	CTGCTCGGATGCTGATGGGCTGGACCTGCTGTTGTCGCCACAGACCATGTTGGCCAC	420
Db	361	CTGCTCGGATGCTGATGGGCTGGACCTGCTGTTGTCGCCACAGACCATGTTGGCCAC	420
Qy	421	GGACAGAGCGAAGGGAGAGGATGGTGTGCTGACCTTCCACGTTTTCGTGAGGGATGTG	480
Db	421	GGACAGAGCGAAGGGAGAGGATGGTGTGCTGACCTTCCACGTTTTCGTGAGGGATGTG	480
Qy	481	TTGACGATGTGGATTCATGCAAGAACTACCTGGGCTTCCTGTTCTTCCTTCGGGC	540
Db	481	TTGACGATGTGGATTCATGCAAGAACTACCTGGGCTTCCTGTTCTTCCTTCGGGC	540
Qy	541	CACCTCCATGGAGGGCCATCGCCATCTCAGCGCGCAGAGAGCGCGGGCACCTTCGCC	600
Db	541	CACCTCCATGGAGGGCCATCGCCATCTCAGCGCGCAGAGAGCGCGGGCACCTTCGCC	600

Qy	601	GGCATGGTACTCAATTTTCCCTCTGGTCTTTCGCCAATCTGAATCTGCAACAACTTTCAAG	660
Db	601	GGCATGGTACTCAATTTTCCCTCTGGTCTTTCGCCAATCTGAATCTGCAACAACTTTCAAG	660
Qy	661	GTCTTCTGCGAAGGCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCCCCATCGAC	720
Db	661	GTCTTCTGCGAAGGCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCCCCATCGAC	720
Qy	721	TCCAGCGTGTCTCTCGGAATAGACAGAGGTGCAATTTATACTCAGACCCCTCTGATC	780
Db	721	TCCAGCGTGTCTCTCGGAATAGACAGAGGTGCAATTTATACTCAGACCCCTCTGATC	780
Qy	781	TGCGGGCAGGGCTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCCGTCTCAGGGTG	840
Db	781	TGCGGGCAGGGCTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCCGTCTCAGGGTG	840
Qy	841	GAGCGGCCCTCCCAAGCTGACGTGCTCTCTGCTTCCAGGGCTCTGCCGATCGC	900
Db	841	GAGCGGCCCTCCCAAGCTGACGTGCTCTCTGCTTCCAGGGCTCTGCCGATCGC	900
Qy	901	CTATGTGACAGCAAGGGGCTACCTGCTCATGGAGTTAGCCAGAGCCAGCAAGACT	960
Db	901	CTATGTGACAGCAAGGGGCTACCTGCTCATGGAGTTAGCCAGAGCCAGCAAGACT	960
Qy	961	CTCAAGATTTATGAAGGTGCTTACCATGTTCTCCACAAGGAGCTTCCTGAAGTCAACAC	1020
Db	961	CTCAAGATTTATGAAGGTGCTTACCATGTTCTCCACAAGGAGCTTCCTGAAGTCAACAC	1020
Qy	1021	TCCGTCTTCATGAATAAATGAGTGGTCTCTCAAGAGCAGCCAGCGGAGGAACTGCG	1080
Db	1021	TCCGTCTTCATGAATAAATGAGTGGTCTCTCAAGAGCAGCCAGCGGAGGAACTGCG	1080
Qy	1081	TCCCCACCTTGAAATGCAATGCGCGTCCCGGCTCATGGTCTGGGGATGCGAGCAGGG	1140
Db	1081	TCCCCACCTTGAAATGCAATGCGCGTCCCGGCTCATGGTCTGGGGATGCGAGCAGGG	1140
Qy	1141	AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCANAAAAA	1192
Db	1141	AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCANAAAAA	1192

RESULT 3  
ABN96912  
ID ABN96912 standard; DNA; 1192 BP.  
XX AC ABN96912;  
XX AC ABN96912;  
XX DT 13-AUG-2002 (first entry)  
XX DE Gene #3410 used to diagnose liver cancer.  
XX DE Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
XX KW metastatic liver tumor; cytostatic; expression profile; disease state;  
XX KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
XX OS Homo sapiens.  
XX XX W0200229103-A2.  
XX XX 11-APR-2002.  
XX XX 02-OCT-2001; 2001WO-US030589.  
XX XX 02-OCT-2000; 2000US-0237054P.  
XX XX (GENE-) GENE LOGIC INC.  
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
XX DR WPI; 2002-426119/45.  
XX PT Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the

PT Level of expression of two or more genes in a liver tissue sample.

PS Claim 1; SEQ ID NO 3410; 298pp; English.

XX The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytotstatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;

Query Match 100.0%; Score 1192; DB 6; Length 1192;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCGAAAGGACAGGCTCGGGTGGGGAAGAGGCTCGAGCTGCTTCCTGCTGCC 60

Db 1 CCAGCCGAAAGGACAGGCTCGGGTGGGGAAGAGGCTCGAGCTGCTTCCTGCTGCC 60

Qy 61 TTGGGGCGCCGATGAGGAGACAGCCGATTTGCTGCTGCTTCATTTCCAGGCTGTC 120

Db 61 TTGGGGCGCCGATGAGGAGACAGCCGATTTGCTGCTGCTTCATTTCCAGGCTGTC 120

Qy 121 GTGGTTGTGGAATGCAACGCGCAGCACATAATGGAACAGGACCTTGAAGCCCTTCCAGC 180

Db 121 GTGGTTGTGGAATGCAACGCGCAGCACATAATGGAACAGGACCTTGAAGCCCTTCCAGC 180

Qy 181 ATGCCAGAGGAAGTTTCCCGAGCGGACCCCGCAGACATTCCTTACAGGACCTCCCT 240

Db 181 ATGCCAGAGGAAGTTTCCCGAGCGGACCCCGCAGACATTCCTTACAGGACCTCCCT 240

Qy 241 CACCTGTGCAATGACAGCGGACAGTACCTCTTCTGACGTACTGGAACCCACAGGCACA 300

Db 241 CACCTGTGCAATGACAGCGGACAGTACCTCTTCTGACGTACTGGAACCCACAGGCACA 300

Qy 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGACAGCAGTGGCCGCTATGAAGAG 360

Db 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGACAGCAGTGGCCGCTATGAAGAG 360

Qy 361 CTGGCTCGGATGCTGATGGGGCTGACCTGCTGTGTTGCGCCACAGCATGTTGGCCAC 420

Db 361 CTGGCTCGGATGCTGATGGGGCTGACCTGCTGTGTTGCGCCACAGCATGTTGGCCAC 420

Qy 421 GGACAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480

Db 421 GGACAGCGAAGGGGAGAGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480

Qy 481 TTGACGATGTGGATTCCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTTCGGGC 540

Db 481 TTGACGATGTGGATTCCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTTCGGGC 540

Qy 541 CACTCCATGGAGGCGCATGCGCATCTCAGGCGCGCAGAGAGCGGGCAGCTTCGCC 600

Db 541 CACTCCATGGAGGCGCATGCGCATCTCAGGCGCGCAGAGAGCGGGCAGCTTCGCC 600

Qy 601 GGCATGTGACTCATTTCCCTCTGCTTCTGCAATCTGAACTGCAACAACTTTCAAG 660

Db 601 GGCATGTGACTCATTTCCCTCTGCTTCTGCAATCTGAACTGCAACAACTTTCAAG 660

Qy 661 GTCTTGTGCGAAAGTGTCTCAACCTTGTGCTGCGCAAACTTGTCCCTCGGGCCCATCGAC 720

Db 661 GTCTTGTGCGAAAGTGTCTCAACCTTGTGCTGCGCAAACTTGTCCCTCGGGCCCATCGAC 720

Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCACATTTTATACTCAGACCCCTGATC 780

Db 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGGTGCACATTTTATACTCAGACCCCTGATC 780

Qy 781 TCCCGGCGAGGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCGCTCTCACGGGTG 840

Db 781 TCCCGGCGAGGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCGCTCTCACGGGTG 840

Qy 841 GAGCGGCCCTTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTTCGCGATGCG 900

Db 841 GAGCGGCCCTTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTTCGCGATGCG 900

Qy 901 CTATGTGACAGCAAGGGGCTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960

Db 901 CTATGTGACAGCAAGGGGCTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960

Qy 961 CTCAAGATTTATGAAGTGTGCTTACCATGTTTCTCCACAAGGAGCTTCCTGAAGTCACCAAC 1020

Db 961 CTCAAGATTTATGAAGTGTGCTTACCATGTTTCTCCACAAGGAGCTTCCTGAAGTCACCAAC 1020

Qy 1021 TCCGTCTTCCATGAATAAATGATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080

Db 1021 TCCGTCTTCCATGAATAAATGATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080

Qy 1081 TCCCAACCTTGAATGATGCTGCGGGTCCCGGCTCATGGTCTGGGGATGCGAGCAGGG 1140

Db 1081 TCCCAACCTTGAATGATGCTGCGGGTCCCGGCTCATGGTCTGGGGATGCGAGCAGGG 1140

Qy 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTTCGCAAAAAA 1192

Db 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTTCGCAAAAAA 1192

RESULT 4

ABS59530

ID ABS59530 standard; cDNA; 1192 BP.

XX

AC ABS59530;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human cDNA, designated SEC9.

XX

Human; gene; ss; SEC; NOV; immunosuppressive; hepatotropic; antiinflammatory; angiotenic-associated disorder; diagnostic; gene therapy; developmental disorder; immune disease; signal transduction pathway disorder; metabolic disorder; feeding disorder; obesity; wasting disorder; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; behavioural disorder; asthma; atherosclerosis; cardiomyopathy; angina pectoris; autoimmune disease; retinal disease; cirrhosis; diabetes; infectious disease; human immunodeficiency virus; HIV; cancer; hypertension; hypotension; multiple sclerosis; urinary retention; osteoporosis; Crohn's disease; ulcer; neurological disorder; anxiety; haemophilia; cirrhosis; immunogen; vaccine.

XX

OS Homo sapiens.

XX

PN WO200255705-A2.

XX

PD 18-JUL-2002.

XX

PF 11-JAN-2002; 2002WO-US000609.

XX

PR 11-JAN-2001; 2001US-0261013P.

PR 11-JAN-2001; 2001US-0261014P.

PR 11-JAN-2001; 2001US-0261018P.

PR 11-JAN-2001; 2001US-0261026P.

PR 11-JAN-2001; 2001US-0261029P.

PR 17-AUG-2001; 2001US-0313170P.

PR 10-SEP-2001; 2001US-0318410P.

XX



KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;  
 KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;  
 KW mTOR; ds.

OS Homo sapiens.

PN WO2004072265-A2.

XX 26-AUG-2004.

PD 11-FEB-2004; 2004WO-US004118.

PF 11-FEB-2003; 2003US-0446133P.

PR 03-APR-2003; 2003US-0459782P.

PR 23-JAN-2004; 2004US-0538246P.

XX (AMHP ) WYETH.

PA (BURC/) BURCZYNSKI M.

PA (TWIN/) TWINE N.

PA (DORN/) DORNER A. J.

PA (TREP/) TREPICCHIO W L.

XX Burczynski M, Twine N, Dornier AJ, Trepicchio WL;

PI WPI; 2004-642301/62.

DR Disclosure; SEQ ID NO 231; 136pp; English.

XX The invention relates to a method of monitoring drug activities in vivo  
 CC by comparing an expression profile of at least one gene in a peripheral  
 CC blood sample of a patient to a reference expression profile of the at  
 CC least one gene, where the at least one gene is differentially expressed  
 CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-  
 CC blood disease and are subjected to a drug therapy as compared to PBMCs  
 CC isolated from the patient before the drug therapy, and where the patient  
 CC has the non-blood disease and is being treated by the drug therapy. The  
 CC method, kit, and nucleic acid array are useful for monitoring drug  
 CC activities in vivo. The drug is especially CCI-779, an ester analogue of  
 CC the immunosuppressant rapamycin (mTOR). This sequence represents a gene  
 CC mammalian target of rapamycin (mTOR). This sequence represents a gene  
 CC expressed in PBMC altered by the drug therapy. (Note: this sequence does  
 CC no form part of the printed specification but was obtained in electronic  
 CC format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences/).

XX Sequence 1192 BP; 262 A; 350 C; 335 G; 245 T; 0 U; 0 Other;

Query Match 100.0%; Score 1192; DB 13; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCCCAAGAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCGCTTCTCGTGGCC 60  
 DB 1 CCAGCCCAAGAGGAGGCTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCGCTTCTCGTGGCC 60

QY 61 TTGGGGCCGCGCAGATGAGGAAACAGCCGATTTGCCGTGTTCTGATTTCCAGGCTGTC 120  
 DB 61 TTGGGGCCGCGCAGATGAGGAAACAGCCGATTTGCCGTGTTCTGATTTCTCAGGCTGTC 120

QY 121 GTGGTTGTGGATGCACACGCCAGACATATGGAACAGGACCTGAAGACCTTCCAGC 180  
 DB 121 GTGGTTGTGGATGCACACGCCAGACATATGGAACAGGACCTTGAAGACCTTCCAGC 180

QY 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 240  
 DB 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 240

QY 241 CACCTGGTCAATGACAGACGACAGTACTCTTCTGCGAGTACTGGAACCCACAGGACCA 300  
 DB 241 CACCTGGTCAATGACAGACGACAGTACTCTTCTGCGAGTACTGGAACCCACAGGACCA 300

QY 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCGCTATGAAGAG 360  
 DB 301 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGAGCACAGTGGCGCTATGAAGAG 360  
 QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTGTTCGCCACAGCACATGTTGGCCAC 420  
 DB 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTGTTCGCCACAGCACATGTTGGCCAC 420  
 QY 421 GGACAGACGAAAGGGGAGAGGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480  
 DB 421 GGACAGACGAAAGGGGAGAGGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480  
 QY 481 TTGCAGCATGTGGATTCATGCAAGAACATACCTGGGCTTCTGTCTTCTTCTTGGCC 540  
 DB 481 TTGCAGCATGTGGATTCATGCAAGAACATACCTGGGCTTCTGTCTTCTTCTTGGCC 540  
 QY 541 CACTCCATGGAGGCGGCATCGCCATCTCAAGCCGCGAGAGAGCGGGGCACTTTCGCC 600  
 DB 541 CACTCCATGGAGGCGGCATCGCCATCTCAAGCCGCGAGAGAGCGGGGCACTTTCGCC 600  
 QY 601 GGCAATGTACTCATTTTCGCTCTGGTCTTGGCCAATCTGAACTCTGCAACAACTTCAAG 660  
 DB 601 GGCAATGTACTCATTTTCGCTCTGGTCTTGGCCAATCTGAACTCTGCAACAACTTCAAG 660  
 QY 661 GTCCCTTCTGCGAAAGTGCTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720  
 DB 661 GTCCCTTCTGCGAAAGTGCTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720  
 QY 721 TCCAGCGTGTCTCTCGGAAATAAGACAGAGGTTCACATTTTATAACTCAGACCCCTGATC 780  
 DB 721 TCCAGCGTGTCTCTCGGAAATAAGACAGAGGTTCACATTTTATAACTCAGACCCCTGATC 780  
 QY 781 TGCCGGCAGGCGTGAAGGTGTCTTCGGCATCCAACTGTGTAATGCCGTCTCAAGGTTG 840  
 DB 781 TGCCGGCAGGCGTGAAGGTGTCTTCGGCATCCAACTGTGTAATGCCGTCTCAAGGTTG 840  
 QY 841 GAGCGCGCTTCCCGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 841 GAGCGCGCTTCCCGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 QY 901 CTATGTGACAGCAAGGGGCTCACTGCTCATGTAGTGTAGCAAGAGCAGGACCAAGACT 960  
 DB 901 CTATGTGACAGCAAGGGGCTCACTGCTCATGTAGTGTAGCAAGAGCAGGACCAAGACT 960  
 QY 961 CTCAGATTTATGAAGTGCCTACCATGTTCTCCAAAGGAGCTTCTGTAAGTCAACAC 1020  
 DB 961 CTCAGATTTATGAAGTGCCTACCATGTTCTCCAAAGGAGCTTCTGTAAGTCAACAC 1020  
 QY 1021 TCCGCTTTCATGAATAAATCAATGTGGTCTCTCAAGAGCAGCCAGGAGGAACCTGCG 1080  
 DB 1021 TCCGCTTTCATGAATAAATCAATGTGGTCTCTCAAGAGCAGCCAGGAGGAACCTGCG 1080  
 QY 1081 TCCCAACCTTGAATGCAATGTCGCGGTGCGCGGTTCATGTTCTGGGGATGACGAGGGG 1140  
 DB 1081 TCCCAACCTTGAATGCAATGTCGCGGTGCGCGGTTCATGTTCTGGGGATGACGAGGGG 1140  
 QY 1141 AAGGGCAGAGATGCGCTTCTCAGATATGCTTGTGCAAAAAA 1192  
 DB 1141 AAGGGCAGAGATGCGCTTCTCAGATATGCTTGTGCAAAAAA 1192

RESULT 6

ADRI4672

ID ADRI4672 standard; DNA; 1582 BP.

XX ADRI4672;

XX AC

XX 21-OCT-2004 (first entry)

XX DT

XX DE

XX Human NF-kappaB pathway-associated gene SeqID673.

XX KW

NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;



antiarthritic; anti-rheumatic; gastrointestinal-Gen; antiasthmatic;  
 antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
 immunosuppressive; vulnerary; gene therapy; immune disorder;  
 inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
 X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
 viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
 viral replication; host cell survival; evasion of immune response;  
 rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
 atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 autoimmune disorder; hyper immune activity;  
 aberrant acute phase response; hypercongenital condition; birth defect;  
 necrotic lesion; wound; organ transplant rejection;  
 aberrant signal transduction; proliferating disorder; cancer;  
 HIV propagation; gene; ds; human.

Homo sapiens.

WO2004065577-A2.

05-AUG-2004.

13-JAN-2004; 2004WO-US000798.

14-JAN-2003; 2003US-0440068P.

12-MAY-2003; 2003US-0469757P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Nadler SG, Neubauer MG, Feder JN, Carman J;  
 WPI: 2004-562168/54.  
 P-PSDB; ADR14673.

New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.

Claim 1; SEQ ID NO 673; 237pp; English.

This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an anti-inflammatory, cytostatic, hepatotropic, virucide, antiarthritic, anti-rheumatic, gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, cancer, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.

Seq Sequence 1582 BP; 336 A; 464 C; 463 G; 319 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 1192; DB 13; Length 1582;

Pred. No. 0;

	Matches	1192;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CCAGCCCGAAGGAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC	60							
Db	379	CCAGCCCGAAGGAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC	438							
Qy	61	TTGGGGCGCCCGAGATGAGGAAACAGCCCGATTTGCTGTTCTGATTTCTCCAGGCTGTC	120							
Db	439	TTGGGGCGCCCGAGATGAGGAAACAGCCCGATTTGCTGTTCTGATTTCTCCAGGCTGTC	498							
Qy	121	GTGGTTGTGGAATGCAACCGCAGCACAATATGAAACAGAGACCTGAAGACCTTCCAGC	180							
Db	499	GTGGTTGTGGAATGCAACCGCAGCACAATATGAAACAGAGACCTTGAAGACCTTCCAGC	558							
Qy	181	ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGAGACTCCCT	240							
Db	559	ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGAGACTCCCT	618							
Qy	241	CACCTGGTCAATGCAGACGAGACAGTACCTCTTCTGAGGTACTGGAACCCACAGGCACA	300							
Db	619	CACCTGGTCAATGCAGACGAGACAGTACCTCTTCTGAGGTACTGGAACCCACAGGCACA	678							
Qy	301	CCCAAGGCCCTCATCTTTTGTGTCATGAGCCGAGAGACAGTGGCCGCTATGAAGAG	360							
Db	679	CCCAAGGCCCTCATCTTTTGTGTCATGAGCCGAGAGACAGTGGCCGCTATGAAGAG	738							
Qy	361	CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCAGTGGGCCAC	420							
Db	739	CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCAGTGGGCCAC	798							
Qy	421	GGACAGAGCGAAGGGGAGAGGATGTTAGTGTCTGACCTTCCACGTTTTCGTGAGGATGTG	480							
Db	799	GGACAGAGCGAAGGGGAGAGGATGTTAGTGTCTGACCTTCCACGTTTTCGTGAGGATGTG	858							
Qy	481	TTGAGCATGTGATTCATGTCGAGAAAGACTACCTGGGCTTCTGCTCTCTTCTGCGGC	540							
Db	859	TTGAGCATGTGATTCATGTCGAGAAAGACTACCTGGGCTTCTGCTCTCTTCTGCGGC	918							
Qy	541	CACCTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGGCGGGGCGCTTGGCC	600							
Db	919	CACCTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGGCGGGGCGCTTGGCC	978							
Qy	601	GGCATGTACTCATTTTCGCTCTGTTTCTTGGCAATCTTGAATCTGCAACAACTTCAAG	660							
Db	979	GGCATGTACTCATTTTCGCTCTGTTTCTTGGCAATCTTGAATCTGCAACAACTTCAAG	1038							
Qy	661	GTCTTCTCGGAAAGTGCTCAACCTTGTGCTGCAAACTTGTCTCGGGCCCATCGAC	720							
Db	1039	GTCTTCTCGGAAAGTGCTCAACCTTGTGCTGCAAACTTGTCTCGGGCCCATCGAC	1098							
Qy	721	TCCAGCGTCTCTCGGAATAAGAGAGGTGACATTTTAACTCAGACCCCTGATC	780							
Db	1099	TCCAGCGTCTCTCGGAATAAGAGAGGTGACATTTTAACTCAGACCCCTGATC	1158							
Qy	781	TGCGGCGAGGCTGAGAGTGTCTTCCGATCCAACTGCTGAATGCGCTCTCACGGGTG	840							
Db	1159	TGCGGCGAGGCTGAGAGTGTCTTCCGATCCAACTGCTGAATGCGCTCTCACGGGTG	1218							
Qy	841	GAGCGGCCCTCCCAAGTGTGCTTCTGCTGCTCCAGGGCTCTGCGCATGCG	900							
Db	1219	GAGCGGCCCTCCCAAGTGTGCTTCTGCTGCTCCAGGGCTCTGCGCATGCG	1278							
Qy	901	CTATGTGACGAAAGGGGCTTACCTGCTCATGGAGTTAGCAAGCCAGGACAAGACT	960							
Db	1279	CTATGTGACGAAAGGGGCTTACCTGCTCATGGAGTTAGCAAGCCAGGACAAGACT	1338							
Qy	961	CTAAGATTATGAAGTGTCTTACCAAGAGGCTTCTGAAGTCAACAAC	1020							
Db	1339	CTAAGATTATGAAGTGTCTTACCAAGAGGCTTCTGAAGTCAACAAC	1398							
Qy	1021	TCCGTCTTCCATGAAATAAATGTGGTCTCTCAAGGACAGCCAGGAGAACTGCG	1080							
Db	1399	TCCGTCTTCCATGAAATAAATGTGGTCTCTCAAGGACAGCCAGGAGAACTGCG	1458							

QY 1081 TCCCACCCCTGAATGCATTGGCCGGTGCCTGGCTCATGGTCTGGGGATGCAGCAGGG 1140  
Db 1459 TCCCACCCCTGAATGCATTGGCCGGTGCCTGGCTCATGGTCTGGGGATGCAGCAGGG 1518  
QY 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1192  
Db 1519 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1570  
RESULT 7  
ADP24423  
ID ADP24423 standard; cDNA; 1582 BP.  
XX  
AC ADP24423;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE PRO polypeptide encoding cDNA SEQ ID NO:1601.  
XX  
KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;  
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
KW gene therapy; immune system.  
XX  
OS Unidentified.  
XX  
FN WO2004041170-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034312.  
XX  
PR 01-NOV-2002; 2002US-0423394P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;  
PI Wu TD;  
XX  
XX WPI; 2004-419628/39.  
DR P-PSDB; ADP24424.  
XX  
XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
PS Claim 1; SEQ ID NO 1601; 2940pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, Gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence encodes a PRO protein of  
CC the invention.  
XX  
SQ Sequence 1582 BP; 336 A; 464 C; 463 G; 319 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1192; DB 13; Length 1582;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCAGCCCGAAAGCAGGGTCTGGGTGCGGAAGAGGGCTCGAGCTGCCTTCTGTGTC 60  
Db 379 CCAGCCCGAAAGCAGGGTCTGGGTGCGGAAGAGGGCTCGAGCTGCCTTCTGTGTC 438  
QY 61 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTGCTGCTGTGATTCAGGCTGTC 120  
Db 439 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTGCTGCTGTGATTCAGGCTGTC 498  
QY 121 GTGGTTGTGGAATGCAAAACCCAGACATATGGAACAGGACCTGAAGACCTTCAGC 180  
Db 499 GTGGTTGTGGAATGCAAAACCCAGACATATGGAACAGGACCTGAAGACCTTCAGC 558  
QY 181 ATGCCAGAGAAAGTTCCCCAGCGGACCCCGCAGAGCATTCCTTACCAGGACCTCCCT 240  
Db 559 ATGCCAGAGAAAGTTCCCCAGCGGACCCCGCAGAGCATTCCTTACCAGGACCTCCCT 618  
QY 241 CACTGTGTAATGCAGACGGACAGTACCTCTTCTGAGGTACTGGAAACCCAGAGGACA 300  
Db 619 CACTGTGTAATGCAGACGGACAGTACCTCTTCTGAGGTACTGGAAACCCAGAGGACA 678  
QY 301 CCCAAGCCCTCATCTTTGTGTCCTGAGCGGAGACAGACAGTGGCCGCTATGAAGAG 360  
Db 679 CCCAAGCCCTCATCTTTGTGTCCTGAGCGGAGACAGACAGTGGCCGCTATGAAGAG 738  
QY 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGTGTTCCGCCACGACCATTTGGCCAC 420  
Db 739 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGTGTTCCGCCACGACCATTTGGCCAC 798  
QY 421 GGACAGAGCGAAAGGGAGAGATGGTAGTGTGTGACTTCCACGTTTTGTCGAGGATGTG 480  
Db 799 GGACAGAGCGAAAGGGAGAGATGGTAGTGTGTGACTTCCACGTTTTGTCGAGGATGTG 858  
QY 481 TTGCAGCATGTGATTTCCATGCGAAGAGACTACCTGGGGTTCCTGCTTCTTCTGGGC 540  
Db 859 TTGCAGCATGTGATTTCCATGCGAAGAGACTACCTGGGGTTCCTGCTTCTTCTGGGC 918  
QY 541 CACTCCATGGGAGGCGCCATCGCCATCTCTCA CGGCCGAGAGAGCGGGCCACTTCGCC 600  
Db 919 CACTCCATGGGAGGCGCCATCGCCATCTCTCA CGGCCGAGAGAGCGGGCCACTTCGCC 978  
QY 601 GGCATGTGACTCAATTTGCGCTCTGGTTCTTGGCCAACTCCTGAATGCAACACTTCAAG 660  
Db 979 GGCATGTGACTCAATTTGCGCTCTGGTTCTTGGCCAACTCCTGAATGCAACACTTCAAG 1038  
QY 661 GTCCTTCTCGGAAAGTCTCAACTTGTGCTGCCAACTTGTCCCTCGGGCCCATCGAC 720  
Db 1039 GTCCTTCTCGGAAAGTCTCAACTTGTGCTGCCAACTTGTCCCTCGGGCCCATCGAC 1098  
QY 721 TCCAGCGCTGCTCTCTCGGAATAGACAGAGGTGACATTTATTA CTACAGACCCCTGATC 780  
Db 1099 TCCAGCGCTGCTCTCTCGGAATAGACAGAGGTGACATTTATTA CTACAGACCCCTGATC 1158  
QY 781 TGC CGGCGAGGGCTGAAGGTGTGTTCTGGGATCCAACTGCTGAATGCGTCTCAGGGGTG 840  
Db 1159 TGC CGGCGAGGGCTGAAGGTGTGTTCTGGGATCCAACTGCTGAATGCGTCTCAGGGGTG 1218  
QY 841 GAGCGCCCTCCCAAGCTGACTGTGCCCTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900  
Db 1219 GAGCGCCCTCCCAAGCTGACTGTGCCCTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 1278  
QY 901 CTATGTGACAGCAAGGGGCTTACCTCTCATGAGTTAGCCAAAGAGCCAGGACAAGACT 960

Db 1279 CTATGTGACAGCAAGGGGCTTACCTGCTCATGTGAGTTAGCCAGAGCCAGCAGAACT 1338  
QY 961 CTCAAGATTATGAAGGTGCTTACCATTGTTCTCCACAGGAGCTTCTCTGAAGTCAACCAAC 1020  
Db 1339 CTCAAGATTATGAAGGTGCTTACCATTGTTCTCCACAGGAGCTTCTCTGAAGTCAACCAAC 1398  
QY 1021 TCCGTCCTTCCATGAATAAATCAATGTGGGTCTCTCAAGAGCAGCCACGGCAGGAACCTCG 1080  
Db 1399 TCCGTCCTTCCATGAATAAATCAATGTGGGTCTCTCAAGAGCAGCCACGGCAGGAACCTCG 1458  
QY 1081 TCCCCACCTGAATGCATTGGCCGCTGCGCGCTCATGCTCTGGGGATGCGAGCAGGG 1140  
Db 1459 TCCCCACCTGAATGCATTGGCCGCTGCGCGCTCATGCTCTGGGGATGCGAGCAGGG 1518  
QY 1141 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1192  
Db 1519 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1570  
  
RESULT 8  
ADO39191  
ID ADO39191 standard; cDNA; 1192 BP.  
XX ADO39191;  
AC ADO39191;  
DT 15-JUL-2004 (first entry)  
XX Human cDNA encoding novel secreted protein SEC9.  
DE  
XX Human; ss; gene; secreted protein; SECX; cardiomyopathy; atherosclerosis;  
KW hypertension; congenital heart defect; aortic stenosis;  
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;  
KW valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;  
KW congenital adrenal hyperplasia; prostate cancer; neoplasm;  
KW adenocarcinoma; lymphoma; uterus cancer; haemophilia; hypercoagulation;  
KW idiopathic thrombocytopaenic purpura; immunodeficiency;  
KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;  
KW multiple sclerosis; angiogenic-associated disorder; psoriasis;  
KW wound healing; stroke.  
XX Homo sapiens.  
XX  
XX US2004018196-A1.  
XX  
PD 29-JAN-2004.  
XX  
XX 11-JAN-2002; 2002US-00044564.  
XX  
XX 11-JAN-2001; 2001US-0261013P.  
PR 11-JAN-2001; 2001US-0261014P.  
PR 11-JAN-2001; 2001US-0261018P.  
PR 11-JAN-2001; 2001US-0261026P.  
PR 11-JAN-2001; 2001US-0261029P.  
PR 17-AUG-2001; 2001US-0313170P.  
PR 10-SEP-2001; 2001US-0318410P.  
XX  
XX (MEZE/) MEZES P D.  
PA (RAST/) RASTELLI L.  
PA (HERR/) HERRMANN J L.  
PA (MACD/) MACDOUGALL J R.  
PA (ZHON/) ZHONG H.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOS F L.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (EISE/) EISEN A J.  
PA (SPAD/) SPADERNA S K.  
PA (VERN/) VERNET C A M.  
PA (BERG/) BERGHS C.  
PA (SPYT/) SPYTEK K A.  
PA (DIP/) DIPIPPO V A.  
PA (ZBRH/) ZERHUSEN B D.

PA (PEYM/) PEYMAN J A.  
PA (ELLE/) ELLERMAN K.  
PA (STON/) STONE D J.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
PA (EDIN/) EDINGER S R.  
XX  
PI Mezes PD, Rastelli L, Herrmann JL, Macdougall JR, Zhong H;  
PI Casman SJ, Boldog FL, Shimkets RA, Gorman L, Eisen AJ, Spaderna SK;  
PI Vernet CAM, Berghs C, Spytek KA, Dipippo VA, Zerhusen BD, Peyman JA;  
PI Ellerman K, Stone DJ, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK;  
PI Burgess CB, Edinger SR;  
XX  
DR WPI; 2004-121988/12.  
DR P-PSDB; ADO39192.  
XX  
XX New isolated SECX polypeptides and polynucleotides, useful for treating  
or preventing, e.g. cardiomyopathy, atherosclerosis, obesity, prostate  
cancer, hemophilia, graft versus host disease, Crohn's disease, multiple  
sclerosis or psoriasis.  
XX  
XX Disclosure; SEQ ID NO 17; 306pp; English.  
XX  
XX The invention relates to a method of treating or delaying the onset of an  
angiogenic-associated disorder comprising administering an antibody to  
the polypeptide of SEC1. The cDNAs and proteins for SEC1-SEC12 are  
disclosed as new. Also included are an isolated NOVX (NOV1-NOV8)  
polypeptide (or its mature form or variant), the encoding nucleic acid  
for the NOVX protein described above, a vector comprising the nucleic  
acid molecule, a cell comprising the vector, an antibody that binds  
immunologically to NOVX, a method of treating or delaying the onset of  
an angiogenic-associated disorder, a method for determining the presence  
of or predisposition to a disease associated with altered levels of SEC1  
(or altered levels of the nucleic acid of SEC1 in a first mammalian  
subject), a method for determining the presence of or predisposition to a  
disease associated with altered levels of SEC1-SEC12, a method of  
treating a pathological state in a mammal, a method of treating or  
delaying the onset of a disorder, a method for determining the presence  
or amount of the polypeptide or nucleic acid, a method of identifying an  
agent that binds to a polypeptide, a method for identifying an agent that  
modulates the expression or activity of the polypeptide, a method for  
modulating the activity of the polypeptide, a method of treating or  
preventing a SECX-associated or NOVX disorder, a pharmaceutical  
composition (comprising NOVX or SECX, the nucleic acid molecule or the  
antibody and a pharmaceutical carrier), a kit comprising (in one or more  
containers) the pharmaceutical composition and a method for determining  
the presence of or predisposition to a disease associated with altered  
levels of the polypeptide or the nucleic acid in a first mammalian  
subject. The SECX/NOVX polypeptides and polynucleotides are useful for  
cardiomyopathy, atherosclerosis, hypertension, congenital heart defects,  
aortic stenosis, atrial septal defect, atrioventricular canal defect,  
ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular  
septal defect, valve disease, tuberosus sclerosis, scleroderma, obesity,  
transplantation, congenital adrenal hyperplasia, prostate cancer,  
neoplasm, adenocarcinoma, lymphoma, uterus cancer, haemophilia,  
hypercoagulation, idiopathic thrombocytopaenic purpura,  
immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,  
Crohn's disease or multiple sclerosis. They are also useful for treating  
angiogenic-associated disorders including psoriasis, wound healing or  
stroke. The present sequence encodes a SECX protein.  
XX  
SQ Sequence 1192 BP; 262 A; 349 C; 335 G; 245 T; 0 U; 1 Other;  
  
Query Match 99.9%; Score 1191; DB 12; Length 1192;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1191; Conservative 0; Mismatches 1; Indels. 0; Gaps 0;  
  
QY 1 CCAGCCCGAAAGCAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60  
Db 1 CCAGCCCGAAAGCAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60

Qy 61 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTTGCCTGGTTCTGATTTCTCCAGGCTGTC 120  
Db 61 TTGGGGCCGCCAGATGAGGGAACAGCCCGATTTTGCCTGGTTCTGATTTCTCCAGGCTGTC 120  
  
Qy 121 GTGGTTGTGGAATGCAACCGCAGCACATAATGGAACAGGACCTGAAGACCCCTTCCAGC 180  
Db 121 GTGGTTGTGGAATGCAACCGCAGCACATAATGGAACAGGACCTGAAGACCCCTTCCAGC 180  
  
Qy 181 ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTCCTTACGAGGACTCCCT 240  
Db 181 ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGAGAGCATTCCTTACGAGGACTCCCT 240  
  
Qy 241 CACCTGGTCAATGCAGCGGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300  
Db 241 CACCTGGTCAATGCAGCGGACAGTACCTCTTCTGCAGGTACTGGAACCCACAGGCACA 300  
  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGACAGTGGCGGCTATGAAGAG 360  
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCGGAGACAGTGGCGGCTATGAAGAG 360  
  
Qy 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTTGGCCACGACCATGTTGGCCAC 420  
Db 361 CTGGCTCGGATGCTGATGGGCTGGACCTGTGTGTTTGGCCACGACCATGTTGGCCAC 420  
  
Qy 421 GGACAGAGCGAAGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTCAAGGATGTG 480  
Db 421 GGACAGAGCGAAGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTCAAGGATGTG 480  
  
Qy 481 TTGCAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGTCTTCTTCTGGGC 540  
Db 481 TTGCAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGTCTTCTTCTGGGC 540  
  
Qy 541 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCGAGAGAGCGCGGCGCACTTGGCC 600  
Db 541 CACTCCATGGAGGCGCCATCGCCATCTCAAGCGCGAGAGAGCGCGGCGCACTTGGCC 600  
  
Qy 601 GGCATGTGTACTCATTTGCGCTCTGGTTCTGCCAATCTGGAATCTGCAACAACTTCAAG 660  
Db 601 GGCATGTGTACTCATTTGCGCTCTGGTTCTGCCAATCTGGAATCTGCAACAACTTCAAG 660  
  
Qy 661 GTCCTTGTGCGAAAGTGTCTCAACCTGTGTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720  
Db 661 GTCCTTGTGCGAAAGTGTCTCAACCTGTGTGTGTCGCAAACTTGTCCCTCGGCGCCATCGAC 720  
  
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATACTCAGACCCCTGTATC 780  
Db 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTATACTCAGACCCCTGTATC 780  
  
Qy 781 TGCCGGGCGAGGCTGCAAGTGTGTTGGGCATCCAACTGCTGAATCGCGTCTCAGCGGTG 840  
Db 781 TGCCGGGCGAGGCTGCAAGTGTGTTGGGCATCCAACTGCTGAATCGCGTCTCAGCGGTG 840  
  
Qy 841 GAGCGCGCCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900  
Db 841 GAGCGCGCCTCCCCAAGCTGACTGTGCGCTTCTCTGCTGCTCCAGGGCTCTGCCGATCGC 900  
  
Qy 901 CTATGTGACAGCAAGGGCCCTA CTGTCTCATGAGTTAGCCAGAGCAGGACAAGACT 960  
Db 901 CTATGTGACAGCAAGGGCCCTA CTGTCTCATGAGTTAGCCAGAGCAGGACAAGACT 960  
  
Qy 961 CTCAGATTTATGAGTGCTTACCATGTTCTCCACAGGAGCTTCTGAAGTCAACAC 1020  
Db 961 CTCAGATTTATGAGTGCTTACCATGTTCTCCACAGGAGCTTCTGAAGTCAACAC 1020  
  
Qy 1021 TCCGCTCTTCCATGAAATAAATGTGGTCTCTCAAGGACAGGCAAGGAGAACTGCG 1080  
Db 1021 TCCGCTCTTCCATGAAATAAATGTGGTCTCTCAAGGACAGGCAAGGAGAACTGCG 1080  
  
Qy 1081 TCCCCACCTGAAATGCATTTGGCGGCTGCGCGGCTCATGGTCTGGGGGATGACGAGGG 1140  
Db 1081 TCCCCACCTGAAATGCATTTGGCGGCTGCGCGGCTCATGGTCTGGGGGATGACGAGGG 1140

Qy 1141 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1192  
Db 1141 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAA 1192  
  
RESULT 9  
ADL56807  
ID ADL56807 standard; cDNA; 1192 BP.  
XX ADL56807;  
AC ADL56807;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human SEX cDNA #9.  
XX  
KW Human; SEX; gene; ss; angiogenic-associated disorder; cancer;  
KW cardiovascular disease; psoriasis; wound healing; stroke; cardiomyopathy;  
KW atherosclerosis; cell signal processing disorder;  
KW metabolic pathway modulation disorder; diabetes;  
KW hyperproliferative disease; cirrhosis; keloid; psoriasis; osteoarthritis;  
KW haemorrhage; ischaemic heart disease; renal disease; thrombosis;  
KW hypertension; hypothyroidism; autoimmune disorder; multiple sclerosis;  
KW systemic lupus erythematosus; rheumatoid arthritis;  
KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;  
KW autoimmune thyroiditis; myasthenia gravis; graft-versus-host disease;  
KW asthma, periodontal disease; Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease; amyotrophic lateral sclerosis; shy-drager syndrome.  
XX  
OS Homo sapiens.  
XX  
PN US2003215449-A1.  
XX  
PD 20-NOV-2003.  
XX  
PF 15-MAR-2002; 2002US-00099322.  
XX  
PR 11-JAN-2001; 2001US-0261013P.  
PR 11-JAN-2001; 2001US-0261014P.  
PR 11-JAN-2001; 2001US-0261018P.  
PR 11-JAN-2001; 2001US-0261026P.  
PR 11-JAN-2001; 2001US-0261029P.  
PR 23-MAR-2001; 2001US-0278152P.  
PR 17-AUG-2001; 2001US-0313170P.  
PR 10-SEP-2001; 2001US-0318410P.  
PR 11-JAN-2002; 2002US-00044564.  
XX  
PA (MEZE/) MEZES P D.  
PA (RAST/) RASTELLI L.  
PA (HERR/) HERRMANN J L.  
PA (MACD/) MACDOUGALL J R.  
PA (ZHON/) ZHONG H.  
PA (CASW/) CASMAN S J.  
PA (BOLD/) BOLDOS F L.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (EISE/) EISEN A J.  
PA (SPAD/) SPADERNA S K.  
PA (VERN/) VERNET C A M.  
PA (BERG/) BERGS C.  
PA (SPYT/) SPYTEK K A.  
PA (DIP1/) DIPIPO V A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PEYW/) PEYMAN J A.  
PA (ELLE/) ELLERMAN K.  
PA (STON/) STONE D J.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
PA (EDIN/) EDINGER S R.  
PA (VOSS/) VOSS E Z.  
PA (MILL/) MILLER C E.

XX Mezes PD, Rastelli L, Herrmann JL, Macdougall JR, Zhong H;  
PI Casman SJ, Boldog FL, Shimkets RA, Gorman L, Eisen AJ, Spaderna SK;  
PI Vernet KM, Berghs C, Spytek KA, Dipippo VA, Zerhusen BD, Peyman JA;  
PI Ellerman K, Stone DJ, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK;  
PI Burgess CE, Edinger SR, Voss EZ, Miller CE;  
XX WPI; 2004-130990/13.  
DR P-ESDB; ADL56808.  
XX  
XX Novel isolated SEC1 and/or NOVX polypeptide, useful for treating cancer,  
PT cardiovascular disease, psoriasis, wound healing, and stroke.  
PT  
XX Disclosure; SEQ ID NO 17; 315pp; English.  
XX  
XX The invention relates to human SECX and NOVX polypeptides and the  
CC polynucleotides encoding them. The invention also relates to antibodies  
CC that bind immunospecifically to the polypeptides. The sequences are  
CC useful for treating or preventing angiogenic-associated disorders,  
CC cancer, cardiovascular disease, psoriasis, wound healing, stroke,  
CC cardiomyopathy, atherosclerosis, cell signal processing disorders,  
CC metabolic pathway modulation disorders, diabetes, hyperproliferative  
CC diseases, cirrhosis, keloids, psoriasis, osteoarthritis, atherosclerotic  
CC plaque formation, haemorrhage, ischaemic heart disease, renal disease,  
CC thrombosis, hypertension, hypothyroidism, autoimmune disorders, multiple  
CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune  
CC pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis,  
CC myasthenia gravis, graft-versus-host disease, asthma, periodontal  
CC disease, Alzheimer's disease, Parkinson's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis and shy-draeger syndrome. This sequence  
CC represents a human SECX polynucleotide of the invention.  
XX  
SQ Sequence 1192 BP; 262 A; 365 C; 319 G; 245 T; 0 U; 1 Other;

Query Match 97.9%; Score 1167; DB 12; Length 1192;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1176; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CCAGCCGCGGAGGAGGCTCGGGTGGGGAAGAGGGCTCGAGCTGCTTCCTGCTGCC 60  
Db 1 CCAGCCGCGGAGGAGGCTCGGGTGGGGAAGAGGGCTCGAGCTGCTTCCTGCTGCC 60  
Qy 61 TTGGGGCGCGCCAGATGAGGGAACAGCCCGATTTGCTGCTGCTTCAGGCTGTC 120  
Db 61 TTGGGGCGCGCCAGATGAGGGAACAGCCCGATTTGCTGCTGCTTCAGGCTGTC 120  
Qy 121 GTGGTTGTGGAATGCAACGCCAGGACATATGGAACAGAGCCCTGAGACCTTCAGC 180  
Db 121 GTGGTTGTGGAATGCAACGCCAGGACATATGGAACAGAGCCCTGAGACCTTCAGC 180  
Qy 181 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGAGAGCATTCCTACCGAGCTCCCT 240  
Db 181 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGAGAGCATTCCTACCGAGCTCCCT 240  
Qy 241 CACCTGTCTAATGACAGCGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300  
Db 241 CACCTGTCTAATGACAGCGAGTACCTCTTCTGCGAGTACTGGAACCCACAGGCACA 300  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGAGCAGTGGCCGCTATGAAGAG 360  
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTGAGCCGAGAGCAGTGGCCGCTATGAAGAG 360  
Qy 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 421 GGACAGAGCGAAGGGAGAGGATGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 421 GGACAGAGCGAAGGGAGAGGATGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 481 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTGCTGGC 540  
Db 481 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCCTGCTGGC 540

Qy 541 CACTCCATGGAGCGCGCCATCGCCATCCTCA CGGCCGAGAGAGCGCGGCCACTTCGCC 600  
Db 541 CACTCCATGGAGCGCGCCATCGCCATCCTCA CGGCCGAGAGAGCGCGGCCACTTCGCC 600  
Qy 601 GGCATGCTACTCATTTTGGCTCTGCTGCTTTCGCAATCCTGCAATCTGCAACACTTTCAAG 660  
Db 601 GGCATGCTACTCATTTTGGCTCTGCTGCTTTCGCAATCCTGCAATCTGCAACACTTTCAAG 660  
Qy 661 GTCCTTCTGCGAAAGTGCTCAACTTGTGTCGCAAACTTGTCCCTCGGCCCATCGAC 720  
Db 661 GTCCTTCTGCGAAAGTGCTCAACTTGTGTCGCAAACTTGTCCCTCGGCCCATCGAC 720  
Qy 721 TCCAGCGTCTCTCTCGGAATAAGACAGAGGTGACATTTATAACTCAGACCCCTGATC 780  
Db 721 TCCAGCGTCTCTCTCGGAATAAGACAGAGGTGACATTTATAACTCAGACCCCTGATC 780  
Qy 781 TGCCGGCAGGGCTGAAGGTGCTTGGGATCCAACTGCTGATGCTGCTCAAGGCTG 840  
Db 781 TGCCGGCAGGGCTGAAGGTGCTTGGGATCCAACTGCTGATGCTGCTCAAGGCTG 840  
Qy 841 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTCTGCCGATCGC 900  
Db 841 GAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTTCCAGGGCTCTGCCGATCGC 900  
Qy 901 CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960  
Db 901 CTATGTGACAGCAAGGGGCTTACCTGCTCATGAGTTAGCCAGAGCCAGGACAAGACT 960  
Qy 961 CTCAGATTTATGAGGTGCTTACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 961 CTCAGATTTATGAGGTGCTTACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Qy 1021 TCCGCTTTCATGAATAAATGAGTGGTCTCTCAAGAGGACAGCCAGGAGAACTGCG 1080  
Db 1021 TCCGCTTTCATGAATAAATGAGTGGTCTCTCAAGAGGACAGCCAGGAGAACTGCG 1080  
Qy 1081 TCCGCCACCTGAAATGCAATGCGCGGTCGCCGGCTCATGGTCTGGGGGATGCGAGCGGG 1140  
Db 1081 TCCGCCACCTGAAATGCAATGCGCGGTCGCCGGCTCATGGTCTGGGGGATGCGAGCGGG 1140  
Qy 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1192  
Db 1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAAAGAAAAA 1192

RESULT 10  
AAS94886  
ID AAS94886 standard; DNA; 4193 BP.  
XX AAS94886;  
AC AAS94886;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human DNA sequence #141 expressed during foam cell differentiation.  
XX  
KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;  
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200177389-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 04-APR-2001; 2001WO-US011128.  
XX  
XX 05-APR-2000; 2000US-0195106P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;  
PI Tai J;

XX WPI; 2002-010925/01.  
DR  
XX Composition useful for diagnosis of conditions, disorders or diseases  
PT associated with atherosclerosis, comprises several polynucleotides that  
PT are differentially expressed in foam cell development.  
XX  
PS Claim 1; Page 197-198; 315pp; English.  
XX  
CC The present invention relates to the isolation of human polynucleotide  
CC sequences that are differentially expressed during foam cell  
CC differentiation. The polynucleotide sequences of the invention or a  
CC composition comprising these polynucleotides are useful as a high  
CC throughput method for detecting altered expression of one or more  
CC polynucleotides in a sample. The polynucleotides can be used in the  
CC diagnosis of disorders associated with foam cell development such as  
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as  
CC coronary artery disease. The polynucleotide sequences can also be used as  
CC PCR primers and probes. The polynucleotides of the invention are also  
CC useful in gene therapy. AAS94746-AAS95021 represent the human  
CC polynucleotide sequences of the invention which are differentially  
CC expressed during foam cell differentiation  
XX  
SQ Sequence 4193 BP; 904 A; 1264 C; 1116 G; 885 T; 0 U; 24 Other;  
Query Match 97.5%; Score 1162; DB 6; Length 4193;  
Best Local Similarity 99.9%; Pred. No. 3.7e-313;  
Matches 1173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 CCAGCCCCAAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGGAGCTGCTTCCTGCTGCC 60  
Db 452 CCAGCCCCAAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGGAGCTGCTTCCTGCTGCC 511  
Qy 61 TTGGGGCGCCGACGATGAGGAAACAGCCGATTTGCCCTGTTCTGATTTCTCAGGCTGTC 120  
Db 512 TTGGGGCGCCGACGATGAGGAAACAGCCGATTTGCCCTGTTCTGATTTCTCAGGCTGTC 571  
Qy 121 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGCAGCTGAAGACCTTCCAGC 180  
Db 572 GTGGTTGTGGAAATGCAACGCCAGCACATATGGAACAGCAGCTGAAGACCTTCCAGC 631  
Qy 181 ATGCCAGAGGAAGTTCCCGGCGGACCCCGAGAGCATTCCTACCGAGACTCCCT 240  
Db 632 ATGCCAGAGGAAGTTCCCGGCGGACCCCGAGAGCATTCCTACCGAGACTCCCT 691  
Qy 241 CACCTGTCAATGACAGCGACAGTACCTCTCTGCGAGTACT-GGAAACCCACAGGCAC 299  
Db 692 CACCTGTCAATGACAGCGACAGTACCTCTCTGCGAGTACTGCGAAACCCACAGGCAC 751  
Qy 300 ACCCAAGCCCTCATCTTTGTGCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA 359  
Db 752 ACCCAAGCCCTCATCTTTGTGCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA 811  
Qy 360 GCTGCTCGGATGTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCACCATTGTGGCCA 419  
Db 812 GCTGCTCGGATGTGATGGGGCTGGACCTGCTGGTGTTCGCCACAGCACCATTGTGGCCA 871  
Qy 420 CGGACAGAGCGAAAGGGAGAGAGTGGTAGTGTCTGACCTTCCAGCTTTCGTCAGGGATGT 479  
Db 872 CGGACAGAGCGAAAGGGAGAGAGTGGTAGTGTCTGACCTTCCAGCTTTCGTCAGGGATGT 931  
Qy 480 GTTGCAGCATGTGGATTCATGCGAAGAGACTACCTGGGCTTCTGCTTCTCTCTGGG 539  
Db 932 GTTGCAGCATGTGGATTCATGCGAAGAGACTACCTGGGCTTCTGCTTCTCTCTGGG 991  
Qy 540 CCACCTCCATGGAGCGGCATCGCCATCTCTCAGGCCCGCAGAGAGCGCGGCCACTTCGC 599  
Db 992 CCACCTCCATGGAGCGGCATCGCCATCTCTCAGGCCCGCAGAGAGCGCGGCCACTTCGC 1051  
Qy 600 CGGCATGTGACTCATTTTCGCTCTGTTCTGTTGTCGCAATCTCTGAATCTGCAACACTTTCAA 659  
Db 1052 CGGCATGTGACTCATTTTCGCTCTGTTCTGTTGTCGCAATCTCTGAATCTGCAACACTTTCAA 1111

Qy 660 GGTCTTGTGTCGAAAGTGTCTCAACCTTGTGTGTCGCCAACTTGTCTCCCTCGGGCCCATCGA 719  
Db 1112 GGTCTTGTGTCGAAAGTGTCTCAACCTTGTGTGTCGCCAACTTGTCTCCCTCGGGCCCATCGA 1171  
Qy 720 CTCACGCGTCTCTCTCGGAATAAGACAGAGGTGCGACATTTATAAATCAACACCCCTGAT 779  
Db 1172 CTCACGCGTCTCTCTCGGAATAAGACAGAGGTGCGACATTTATAAATCAACACCCCTGAT 1231  
Qy 780 CTGCGCGGACAGGCTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCCCTCTCACGGGT 839  
Db 1232 CTGCGCGGACAGGCTGAAGGTGTCTTCGGCATCCAACTGCTGAATGCCCTCTCACGGGT 1291  
Qy 840 GGAGCGCGCCTCCCAAGTGTGCTGTCCTCTCTCTGCTGCTCCAGGGCTCTGCGGATCG 899  
Db 1292 GGAGCGCGCCTCCCAAGTGTGCTGTCCTCTCTCTGCTGCTCCAGGGCTCTGCGGATCG 1351  
Qy 900 CCTATGTGACAGCAAAAGGGCCCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGAC 959  
Db 1352 CCTATGTGACAGCAAAAGGGCCCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGAC 1411  
Qy 960 TCTCAAGATTTATGAAGTGTCTTACCATGTCTTCCCAAGAGGCTTCTGAGTCAACCAA 1019  
Db 1412 TCTCAAGATTTATGAAGTGTCTTACCATGTCTTCCCAAGAGGCTTCTGAGTCAACCAA 1471  
Qy 1020 CTCGCTCTTCCATGAATAAACAATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAATGCG 1079  
Db 1472 CTCGCTCTTCCATGAATAAACAATGTGGGTCTCTCAAAGGACAGCCACGCGAGGAATGCG 1531  
Qy 1080 GTCCCCACCTGAATGCAATTTGGCGGTGCGCGGTCTATGCTCTGGGGATGCGAGGCAGGG 1139  
Db 1532 GTCCCCACCTGAATGCAATTTGGCGGTGCGCGGTCTATGCTCTGGGGATGCGAGGCAGGG 1591  
Qy 1140 GAAGGCGAGAGATGGCTTCTCAGATATGGCTTGC 1173  
Db 1592 GAAGGCGAGAGATGGCTTCTCAGATATGGCTTGC 1625  
RESULT 11  
ADI21843  
ID ADI21843 standard; cDNA; 1613 BP.  
XX  
AC ADI21843;  
XX  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Novel human protein cDNA #102.  
XX  
XX forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;  
ss; gene.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003025148-A2.  
PN  
XX  
XX 27-MAR-2003.  
PD  
XX  
XX 19-SEP-2002; 2002WO-US029964.  
PP  
XX  
XX 19-SEP-2001; 2001US-0323739P.  
PR  
XX  
XX 13-SEP-2002; 2002US-00323739.  
PR  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Q, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX  
XX WPI; 2003-354603/33.  
DR  
XX P-PSDB; ADI21127.  
DR



XX New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.

XX Claim 1; SEQ ID NO 102; 156pp; English.

CC The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents cDNA encoding a novel human protein.

XX SQ Sequence 1613 BP; 334 A; 465 C; 472 G; 342 T; 0 U; 0 Other;

Query Match 91.9%; Score 1096; DB 10; Length 1613;  
Best Local Similarity 93.8%; Pred. No. 6.1e-295;  
Matches 1184; Conservative 0; Mismatches 0; Indels 78; Gaps 1;

Qy 1 CCAGCCCGAAGGCGGTCTGGGTGCGGGAAGAGGGCTCGAGTGCCTTCCTGCTGCC 60  
Db 352 CCAGCCCGAAGGCGGTCTGGGTGCGGGAAGAGGGCTCGAGTGCCTTCCTGCTGCC 411  
Qy 61 TTGGGCGCCCGATGAGGGAACAGCCCGATTTGCTGTTCTGATTTCTCAGGCTGTC 120  
Db 412 TTGGGCGCCCGATGAGGGAACAGCCCGATTTGCTGTTCTGATTTCTCAGGCTGTC 471  
Qy 121 GTGGTTGTGGAATGCAACGCGCAGCACAATATGGAACAGGACCTTGAAGACCTTCCAGC 180  
Db 472 GTGGTTGTGGAATGCAACGCGCAGCACAATATGGAACAGGACCTTGAAGACCTTCCAGC 531  
Qy 181 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTACCGAGCCTCCCT 240  
Db 532 ATGCCAGAGGAAGTTCCCGCAGGCGGACCCCGCAGAGCATTCCTACCGAGCCTCCCT 591  
Qy 241 CACCTGTCATGACAGCGGACGATACCTCTCTGCGAGTACTGGAACCCACAGGCACA 300  
Db 592 CACCTGTCATGACAGCGGACGATACCTCTCTGCGAGTACTGGAACCCACAGGCACA 651  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCATGAGCGGAGCAGTGGCGGCTATGAGAG 360  
Db 652 CCCAAGGCCCTCATCTTTGTGTCATGAGCGGAGCAGTGGCGGCTATGAGAG 711  
Qy 361 CTGGCTCGGATGCTGATGGGCTGACCTGCTGTTGTCGCCACGACCATGTTGGCCAC 420  
Db 712 CTGGCTCGGATGCTGATGGGCTGACCTGCTGTTGTCGCCACGACCATGTTGGCCAC 771  
Qy 421 GGACAGCGAAGGGAGAGATGATGCTGATCTGATCTCCAGCTTTCGTCAGGAGTGTG 480  
Db 772 GGACAGCGAAGGGAGAGATGATGCTGATCTGATCTCCAGCTTTCGTCAGGAGTGTG 831  
Qy 481 TTGAGCATGTGGATTCATCGCAAGACACTACCTGGGCTTCCTGCTTCCTGCGG 540  
Db 832 TTGAGCATGTGGATTCATCGCAAGACACTACCTGGGCTTCCTGCTTCCTGCGG 891  
Qy 541 CACTCCATGGGAGGCGCCATCGCCATCTCTACGGCCGAGAGAGCGCGGCACTTCGCC 600  
Db 892 CACTCCATGGGAGGCGCCATCGCCATCTCTACGGCCGAGAGAGCGCGGCACTTCGCC 951  
Qy 601 GGCAATGGTACTCATTTTGGCCTCTGGTTCTTGGCAATCTGAACTGCAACAACTTTCAA- 659  
Db 952 GGCAATGGTACTCATTTTGGCCTCTGGTTCTTGGCAATCTGAACTGCAACAACTTTCAA 1011

Qy 660 ----- 659  
Db 1012 GACTATTTCGAGGATTTTGAACACTTGTGAAAAAGGCATCAAGAATGTTAAAGTTTGG 1071  
Qy 660 -----GGTCTTGTGCGAAGTGTCAACCTTGTGTCGCAAACTTG 702  
Db 1072 ATTCACGTCCTTTTGGTCTTGTGCGAAGTGTCAACCTTGTGTCGCAAACTTG 1131  
Qy 703 TCCCTCGGGCCCATCGACTCCAGCGTCTCTCTCGGAATTAAGACAGAGGTGCACTTTAT 762  
Db 1132 TCCCTCGGGCCCATCGACTCCAGCGTCTCTCTCGGAATTAAGACAGAGGTGCACTTTAT 1191  
Qy 763 AACTCAGACCCCTGATCTGCGGGCAGGGGTGAAGTGTGCTTCGGCATCCAACTGCTG 822  
Db 1192 AACTCAGACCCCTGATCTGCGGGCAGGGGTGAAGTGTGCTTCGGCATCCAACTGCTG 1251  
Qy 823 AATGCCGTCTCAGGGTGGAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTC 882  
Db 1252 AATGCCGTCTCAGGGTGGAGCGGCCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTC 1311  
Qy 883 CAGGCTCTGCGGATCGCCTATGTGACAGCAAAAGGGCCCTACCTGCTCATGAGTTAGCC 942  
Db 1312 CAGGCTCTGCGGATCGCCTATGTGACAGCAAAAGGGCCCTACCTGCTCATGAGTTAGCC 1371  
Qy 943 AAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTTACCATGTTTCTCCAAAGGAG 1002  
Db 1372 AAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTTACCATGTTTCTCCAAAGGAG 1431  
Qy 1003 CTTCTGAAAGTACCAACTCCGCTTTCATGAATAAATAACATGTGGGTCTCTCAAAGGACA 1062  
Db 1432 CTTCTGAAAGTACCAACTCCGCTTTCATGAATAAATAACATGTGGGTCTCTCAAAGGACA 1491  
Qy 1063 GCCACGCGAGGACTGCGTCCCACTGATGATGATGCGCGTGGCGGCTCATGTTCT 1122  
Db 1492 GCCACGCGAGGAACTGCGTCCCACTGATGATGATGCGCGTGGCGGCTCATGTTCT 1551  
Qy 1123 GGGGATGTCAGGCGGGAAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAA 1182  
Db 1552 GGGGATGTCAGGCGGGAAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAA 1611  
Qy 1183 AA 1184  
Db 1612 AA 1613

RESULT 12

AAD57495  
ID AAD57495 standard; cDNA; 1309 BP.

XX AAD57495;

XX 20-NOV-2003 (first entry)

XX Human enzyme (ENZM) cDNA #7.

Human; enzyme; ENZM; immune disorder; infection; myocardial infarction;  
gene therapy; anaemia; acquired immune deficiency syndrome; infection;  
reproductive disorder; cardiovascular; eye; cell proliferation; cancer;  
AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence;  
infertility; atherosclerosis; metabolic disorder; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 356..1207  
FT /tag= a  
FT /product= "Human enzyme (ENZM) "

XX WO2003052075-A2.

XX 26-JUN-2003.

XX



BP 12-DEC-2002; 2002WO-US040161.  
XX 14-DEC-2001; 2001US-0340357P.  
PR 20-DEC-2001; 2001US-0342962P.  
PR 21-DEC-2001; 2001US-0343589P.  
PR 22-JAN-2002; 2002US-0351107P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R;  
PI Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;  
PI Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis JP;  
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;  
XX  
XX WPI; 2003-533016/50.  
DR P-PSDB; AAE38215.  
XX  
XX New human enzyme (ENZM) polypeptide, useful for preparing a composition  
PT for treating a disease associated with decreased expression or  
PT overexpression of ENZM e.g. cancer.  
XX  
XX Claim 5; Page 315; 264pp; English.  
XX  
XX The invention relates to human enzyme (ENZM) polypeptides and their  
CC corresponding polynucleotides. ENZM sequences are useful for preparing a  
CC composition for diagnosing or treating a disease or condition associated  
CC with decreased expression or overexpression of functional ENZM. The  
CC disorders include immune disorders (anaemia, allergy or asthma),  
CC infectious disorders (viral, fungal, parasitic or protozoal infection),  
CC immune deficiencies (acquired immune deficiency syndrome; AIDS),  
CC metabolic disorders (Addison's disease, diabetes or goitre), reproductive  
CC disorders (infertility or impotence), cardiovascular disorders  
CC (atherosclerosis or myocardial infarction), eye disorders and cell  
CC proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The  
CC present sequence is human ENZM cDNA  
XX  
XX Sequence 1309 BP; 280 A; 393 G; 395 G; 261 T; 0 U; 0 Other;  
XX  
XX Query Match 84.1%; Score 1002; DB 9; Length 1309;  
XX Best Local Similarity 92.4%; Pred. No. 9.3e-269;  
XX Matches 1102; Conservative 0; Mismatches 0; Indels 90; Gaps 1;  
XX  
XX 1 CCAGCCCAAGGAGGCTCTGGGTGCGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC 60  
XX 206 CCAGCCCAAGGAGGCTCTGGGTGCGGAGAGGGCTCGAGCTGCCTTCCTGCTGCC 265  
XX  
XX 61 TTGGGGCCCGCAGATGAGGAAACAGCCCGGATTTGCCCTGGTTCGATTCTCAGGCTGTC 120  
XX 266 TTGGGGCCCGCAGATGAGGAAACAGCCCGGATTTGCCCTGGTTCGATTCTCAGGCTGTC 325  
XX  
XX 121 GTGGTTGTGGAATGCAACCGCCAGCACATAATGGAACAGAGACCTGAAGACCTTCCAGC 180  
XX 326 GTGGTTGTGGAATGCAACCGCCAGCACATAATGGAACAGAGACCTGAAGACCTTCCAGC 385  
XX  
XX 181 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGAGAGCATTCCTTACCAGACCTCCCT 240  
XX 386 ATGCCAGAGGAAGTTCCTCCAGCGGACCCCGAGAGCATTCCTTACCAGACCTCCCT 445  
XX  
XX 241 CACCTGGTCAATGACAGCGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGACACA 300  
XX 446 CACCTGGTCAATGACAGCGACAGTACCTCTTCTGAGGTACTGGAAACCCACAGGACACA 505  
XX  
XX 301 CCCAAGGCCCTCATCTTTGTGCCATGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 360  
XX 506 CCCAAGGCCCTCATCTTTGTGCCATGAGCCGAGAGCACAGTGGCCGCTATGAAGAG 565  
XX  
XX 361 CTGGCTCGGATGCTGATGGGGCTGACCTGTGGTGTGGCCACGACCATGTTGGCCAC 420  
XX 566 CTGGCTCGGATGCTGATGGGGCTGACCTGTGGTGTGGCCACGACCATGTTGGCCAC 625  
XX  
XX 421 GGACAGAGCGAAGGGGAGAGGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 480  
XX 626 GGACAGAGCGAAGGGGAGAGGATGTTAGTGTCTGACTTCCACGTTTTCGTGAGGATGTG 685

Qy 481 TTGCAGCATGTGATTCATGCGAAGAAGTACCTGGGCTTCTGTGTTCTCTCTCTGGGC 540  
Db 686 TTGCAGCATGTGATTCATGCGAAGAAGTACCTGGGCTTCTGTGTTCTCTCTCTGGGC 745  
Qy 541 CACTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGAGCGCGGCGCACTTCGCGC 600  
Db 746 CACTCCATGGAGGCGCATCGCCATCTCAGCGCCGAGAGAGCGCGGCGCACTTCGCGC 805  
Qy 601 GGCATGCTACTCAATTTTCGCTCTGCTGCTTTCGCAATCTGCAATCTGCAACAACTTTCAAG 660  
Db 806 GGCATGCTACTCAATTTTCGCTCTGCTGCTTTCGCAATCTGCAATCTGCAACAACTTTCA-- 863  
Qy 661 GTCCCTGCTCGGAAAGTGTCTCAACTTGTGCTGCAAACTTGTCCCTCGGGCCCATGCAC 720  
Db 864 ----- 863  
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTGCACATTTTATACTCAGACCCCTGTATC 780  
Db 864 -----AGTGCACATTTTATACTCAGACCCCTGTATC 895  
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XX ADI21842;  
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XX 15-APR-2004 (first entry)  
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XX Novel human protein cDNA #101.  
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XX forensic; nutritional source; damaged tissue; diseased tissue;  
XX myeloid cell disorder; lymphoid cell disorder;  
XX bone cartilage tissue growth; tendon tissue growth;  
XX ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
XX tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;  
XX ss; gene.  
XX  
XX Homo sapiens.  
XX  
XX WO2003025148-A2.  
XX  
XX PD 27-MAR-2003.



OS	Homo sapiens.	
XX	Key	Location/Qualifiers
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FT		/standard_name= "Single nucleotide polymorphism"
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XX	19-SEP-2002.	
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XX	08-MAR-2002; 2002WO-US007288.	
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PR	08-MAR-2001; 2001US-0274281P.	
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PR	03-DEC-2001; 2001US-0338092P.	

PR	04-DEC-2001; 2001US-0337185P.	
PR	03-JAN-2002; 2002US-0345705P.	
PR	08-MAR-2002; 2002US-00093463.	
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PA	(CURA-) CURAGEN CORP.	
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PI	Rastelli L, Mezes PD, Smitheon G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM; Pena CEA, Burgess CE, Liu X, Spytek KA, Gorman L, Spaderna SK; Voss EZ, Malyankar UM, Anderson DW, Patturajan M, Miller CE; Taupier RJ, Padigar M, Shenoy SG, Kekuda R, Gusev VV, Pochart PF; Zhong M;	
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DR	WPI; 2002-732824/79.	
DR	P-PSDH; ABP70136.	
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PT	New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic disorders, and asthma.	
PT		
PT		
XX		
PS	Claim 16; Page 253; 619pp; English.	
XX		
CC	The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABV9327-ABV99595 and ABP70049-ABP70149), where X is any number from 1 to 48. The NOVX proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX coding sequences and proteins are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic disorders, cardiovascular disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disturbances associated with obesity, metabolic syndrome X or wasting disorders associated with chronic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods	
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	Best Local Similarity 90.7%; Pred. No. 3.5e-210;	
	Matches 893; Conservative 0; Mismatches 2; Indels 90; Gaps 1;	
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XX AC ADK68319;
DT 06-MAY-2004 (first entry)
XX DE Human phosphatidase 30.47 cDNA SEQ ID NO:1.
XX KW human; phosphatidase; ds; gene; breast cancer; rheumatoid arthritis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
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FT /*product= "phosphatidase"
XX CN1393553-A.
XX 29-JAN-2003.
XX 29-JUN-2001; 2001CN-00113170.
XX 29-JUN-2001; 2001CN-00113170.
XX PA (BIOW-) BLOWINDOW GENE DEV INC SHANGHAI.
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XX Mao Y, Xie Y;
PI WPI; 2003-422184/40.
DR P-PSDB; ADK68320.
XX Human phosphatidase polypeptide-30.47, encoding polynucleotide,
PT antagonist and recombinant production, useful for treating breast cancer
PT and rheumatoid arthritis.
XX Claim 6; SEQ ID NO 1; 32pp; Chinese.
XX The invention relates to a novel human phosphatidase polypeptide-30.47,
CC the encoding polynucleotide, antagonist and recombinant production. The
CC polypeptide is useful for treating breast cancer and rheumatoid
CC arthritis. The present sequence encodes the human phosphatidase of the
CC invention.
XX Sequence 1450 BP; 363 A; 362 C; 365 G; 360 T; 0 U; 0 Other;
SQ Query Match 65.3%; Score 777.8; DB 10; Length 1450;
Best Local Similarity 96.7%; Pred. No. 3.4e-206;
Matches 794; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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Job time : 679 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	363.4	30.5	517	US-09-621-976-3521	Sequence 3521, Ap
2	183.4	15.4	489	US-09-621-976-126	Sequence 126, App
3	116.2	9.7	4403765	US-09-103-840A-2	Sequence 2, Appli
4	116.2	9.7	4411529	US-09-103-840A-1	Sequence 1, Appli
5	51.2	4.3	402	US-09-060-756-652	Sequence 652, App
6	51.2	4.3	402	US-09-670-314-652	Sequence 652, App
7	48.4	4.1	15572	US-09-902-540-1131	Sequence 1131, Ap
8	43.4	3.6	534	US-09-252-991A-5873	Sequence 5873, Ap
9	43.4	3.6	1968	US-09-252-991A-5829	Sequence 5829, Ap
10	43.4	3.6	2190	US-09-253-991A-5779	Sequence 5779, Ap
11	39	3.3	832	US-09-621-976-2813	Sequence 2813, Ap
12	39	3.3	865	US-09-280-116-63	Sequence 63, Appl
13	39	3.3	1125	US-09-252-991A-11202	Sequence 11202, A
14	38.8	3.3	505	US-09-621-976-15639	Sequence 15639, A
15	38.6	3.2	705	US-09-796-110-3	Sequence 3, Appli
16	38.6	3.2	2830	US-09-010-928B-1	Sequence 1, Appli
17	38.6	3.2	7218	US-08-232-463-14	Sequence 14, Appl
18	38.2	3.2	276	US-09-313-294A-3547	Sequence 3547, Ap
19	38	3.2	1768	US-09-485-529-13	Sequence 13, Appl
20	38	3.2	2125	US-09-485-529-14	Sequence 14, Appl
21	37.8	3.2	789	US-08-602-359A-28	Sequence 28, Appl
22	37.6	3.2	865	US-09-796-110-1	Sequence 1, Appli
23	37.6	3.2	866	US-09-620-312D-482	Sequence 482, App
24	37.4	3.1	6047	US-09-902-540-758	Sequence 758, App
25	37	3.1	8438	US-07-945-283-1	Sequence 1, Appli
26	36.6	3.1	9208	US-09-068-506-1	Sequence 1, Appli
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29	36.4	3.1	1890	4	US-09-252-991A-942	Sequence 942, App
30	36.4	3.1	2001	4	US-09-252-991A-891	Sequence 891, Appl
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32	36.4	3.1	19726	4	US-09-902-540-1164	Sequence 1164, Ap
33	36	3.0	954	4	US-09-252-991A-13383	Sequence 13383, A
34	36	3.0	1057	4	US-09-949-016-4554	Sequence 4554, Ap
35	36	3.0	1430	3	US-09-492-985-1	Sequence 1, Appli
36	36	3.0	1536	4	US-09-252-991A-11693	Sequence 11693, A
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38	36	3.0	49301	4	US-09-949-016-16296	Sequence 16296, A
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ALIGNMENTS

RESULT 1  
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; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3521  
; LENGTH: 517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 291..494  
US-09-621-976-3521

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; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          9.7%; Score 116.2; DB 3; Length 4403765;
Best Local Similarity 48.3%; Pred. No. 3.7e-21;
Matches 356; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

Qy 267 CCTCTCTGCGAGTACGGAACCCACAGGACACCCAGGACCGCCGCGGATGCGTGGGCTGGA 326
Db 214245 CATGCTCTACAGCTCTGGACGCGCGGACACCGCCGCGGATGCGTGGGCTGGA 214304

Qy 327 TGGAGCGGAGAGACAGTGGCGCGCTATGAAGAGCTGGCTCGGATGCGTGGGCTGGA 386
Db 214305 TGGTCTGGCGGAGCATGCGCGCGCTACGACCATGTGCGGAGCGGCTCGGCGGCGG 214364

Qy 387 CTGCTGGTGTTCGCCACGACCATGTTGGCCAGGACAGAGCGGAGGAGAGATGGT 446
Db 214365 CTTGCTCACCTATGCGCTTGACCAACCGCGGCGATGGCGCTCGGCTGGCAACCGG 214424

Qy 447 AGTGTCTGACTTCCACGTTTTCGTACGGGATGTTTGCAGCATGTGGATTCATGCAGAA 506
Db 214425 AGTGAGAGACATCTCCGAGTACACCGCTGACTTCGACACCCCTCGTTGGGATTCG 214484

Qy 507 AGACTACCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 566
Db 214485 GGAATATCCCGGCTGCAAGCGCATCTGCTCGGCGACAGCATGGCGCGCGCATGTG 214544

Qy 567 CTTCACGCGCGCAGAGAGCGCGGCGCACTTCGCGCGCATGTGCTATCTATCTCTCTCT 626
Db 214545 CGCTTACGCTGTGCAACGTCAGACAACTACGACCTGATGCTGTC---TTTCGGCG 214601

Qy 627 TCTTGCCAACTCTGAATCTCAACAACTTTCAAGGCTCTTCTCGGAAAGTCTCAACCT 686
Db 214602 GGTGGCGGCGACAGGACCTGTGTGAGCCCGGTAGTGGCGGTTGCCCGCAAGCTTCT 214661

Qy 687 TGTCTCTCCAACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 746
Db 214662 CGTGGTCCCGGCTGCGCGGTGCGAGAACTGGATTTTACTGCCATCTCTCGCGAC 214721

Qy 747 AGAGTGCAGATTTATTAACCTCAGACCCCTGATCTCGCGGCGAGGCTGAAGTGTG 806
Db 214722 GGTGGTCCAGGCTTACAAACCGACCCGCTGTCGACACGAGCGGTTTCGCGCGG 214781

Qy 807 CGGCATCAACTGCTGAATGCGCTCTCAGGCTGGAGCGCGCTCTCCCAAGCTGACTGT 866
Db 214782 TGGCGCGCGCTGCTGCGAGTGGGCGAGACCATGCGCGGCGGAGCACCGGCATTG 214841

Qy 867 GCCCTTCTCTGCTCTCAGGCGCTCTGCGGATGCGCTATGTGACAGCAAAAGGGCTAC 926
Db 214842 GCCCTGCTAGTGTGACGCGCACCGATGACCGGCTGATCCCCATCAGGCGACCG 214901

Qy 927 GCTCATGAGTTAGCCAAAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGTGCTAC 986
Db 214902 CTTGCTGGAATGTGGGATCGGCGGCGAGCTGAGAGGATATCCCGGCTGTACCA 214961

Qy 987 TGTCTCTCCAGGAGC 1003
Db 214962 CGAGTGTTCACGAGC 214978

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.

Query Match          15.4%; Score 183.4; DB 4; Length 489;
Best Local Similarity 88.6%; Pred. No. 1.9e-42;
Matches 210; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Qy 369 GATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACGACCATGTTGGCCACGACAGAG 428
Db 254 GAAGCGGGGAGCGAGCAGCTGCTGGAAACCCACCTTTTGGCAGTTGGCCACGACAGAG 313

Qy 429 CGAAGGGAGAGAGTGGTAGTCTGACTTCCAGTTTTCGTGAGGAGATGTTGCGACGA 488
Db 314 CGAAGGGAGAGAGTGGTAGTCTGACTTCCACTTTTCGTGAGGAGATGTTGCGACGA 373

Qy 489 TGTGATTCATGACAGAAAGACTACCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 548
Db 374 TGTGATTCATGACAGAAAGACTACCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 433

Qy 549 GGGAGGGCCCATCGCATCTCAGCGCGCGAGAGGCGGGCCACTTTCGCGCGCAT 605
Db 434 GGGAGGGCCCATCG-CATCTCTCAGCGCGCGAGAGGCGGGCCACTTTCGCGCGCAT 489

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
```



```
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match          9.7%; Score 116.2; DB 3; Length 4411529;
Best Local Similarity 48.3%; Pred. No. 3.7e-21; Indels 1; Gaps 1;
Matches 356; Conservative 0; Mismatches 378;

Qy 267 CCTCTTCTGCAGGTACTGGAACCCACAGGCACACCCAAAGCCCTCATCTTTGTGCCCA 326
Db 214136 CATGCTCTACGACGCTGGAGCCGGACACCGCGCGCAAGCGGTGCTGCTGGCCCA 214195

Qy 327 TGGAGCCGAGAGACAGATGCGCCGCTATGAAGAGCTGCTCGATGCTGATGGGCTGGA 386
Db 214196 TGGTCTGGCGGAGCATGCCCGCGCTACGACCATGTGCGCAGCGGCTCGCGCGCGCG 214255

Qy 387 CTTCTGCTGTTCGCCACGACCATGTTGGCCAGCGACAGAGCAGAGGAGAGATGGT 446
Db 214256 CTTGTCACCTATGCTGCTTGACCAACCGCGGCGATGCGCGTTCGGTGGCAACGGGTGCT 214315

Qy 447 AGTGTCTGACTTCCACGCTTTTCGTGAGGATGTGTGCGAGCATGTGGATTCATCGAGAA 506
Db 214316 AGTGAGAGACATCTCGAGTACACCGCTGACTTCGACACCTCTGTTGGATCGCCACCG 214375

Qy 507 AGATACCTCTGGGTTCCTGCTTCCTTCTGGGCACTTCATGGAGCGCGCATGCGCAT 566
Db 214376 GGAATATCCCGGTCGCAAGCGATGCTGCTCGGCGACAGCATGGCGCGCGCATTTGTGT 214435

Qy 567 CTTACGCGCCGACAGAGCGCGGCACTTCGCGGATGTTACTCATTTCCCTCTGCT 626
Db 214436 CGCTTACGGTGTCAACGCTCAGACAACTAGACCTGATGTGC---TTTCGGCGCGCGC 214492

Qy 627 TCTTGCCAACTCTGAATCTGCAACAACTTTCAAGTCTCTGCTGCAAGTGTCTCAACCT 686
Db 214493 GGTGGCGGACAGACCTGTGTGAGCCGGTAGTGGCGGTTCCGCGCAAGCTTCTGGGGT 214552

Qy 687 TGTGCTGCAAACTGTCTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGAC 746
Db 214553 CGTGTGCGCGGCTGCGCGGTGCAAGAACTGATTTTACTGCCATCTCTCGGACCCCTGA 214612

Qy 747 AGAGTTCGACATTTATTAATCAAGCCCTGATCTGCGGCGAGGCTGAAGTGTGCTT 806
Db 214613 GGTGTCCAGCTTTACAAACCGACCCCACTCGTGACACAGGAGGGTTCCGCGCGGGAT 214672

Qy 807 CGGATCCAACTGTGTAATCGCTCTACAGGTGGAGCGCCCTCCCAAGTGAAGTGT 866
Db 214673 TGGCGCGCGTGTCTGAGGTGGGGGAGACCATGCGCGGCGAGCACCGGATTTGACCGC 214732

Qy 867 GCCCTTCTGCTGCTCCAGGCTCTGCGGATCGGCTATGTGACAGCAAGGGGCTACCT 926
Db 214733 GCCGTGCTAGTGTGTCAGCGCACCGGATGACCGGCTGATCCCATCGAGGGCAGCGGTG 214792

Qy 927 CTTATGAGGTAGCAGAGCCAGGACAACTCTCAAGATTTATGAGTGTGCTTACCA 986
Db 214793 CTTGTCGAAATGTGTGGGATCGGCGGACGTGAGGAGTATCCCGGCTGTACCA 214852

Qy 987 TGTCTCCACAGGAGC 1003
Db 214853 CGAGGTGTTCAACGAGC 214869
```

RESULT 5

```
US-09-060-756-652
; Sequence 652, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060.756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 652
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-652

Query Match          4.3%; Score 51.2; DB 3; Length 402;
Best Local Similarity 45.9%; Pred. No. 0.00014;
Matches 152; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 673 AAAGTGTCTAACCTGTGTGTCGCCAAACTGTTCCTCGGGCCCATCGACTCCAGCGTGTCT 732
Db 55 AAGCTTCTGGCGGTGCTGTGTCGCCGCTGCGGTGCGAGAACTGGATTTTACTGCCATC 114

Qy 733 TCTCGAATAAGACAGAGTTCGACATTTATACTCAGACCCCTGATCTGCCGGCGAGG 792
Db 115 TCTCGACACCTGAGGTGGTCCAGGCTTACAACACCGACCCACCTCGTGACACGAGCG 174

Qy 793 CTGAAGTGTGTCTTCGGCATCAACTGCTGAATGCCGTCTCACGGGTGGAGCGGCCCTC 852
Db 175 GTTCCGCGCGGATTTGCCGCGGCTCTGTCANGTGGCGGAGACCATGCGCGCGGAGCA 234

Qy 853 CCCAAGTGTGATGTGCTTCTGCTGCTCCAGGGCTCTGCGCGATCGCTATGTGACAGC 912
Db 235 CCGCATTTGACCGCGCGCTGCTAGTGTGTCAGCGCACCGATGACCGGCTGATCCCCATC 294

Qy 913 AAAGGCGCTTACCTGCTCATGGAGTTAGCCAAGAGCCAGGACAGACTCTCAAGATTTAT 972
Db 295 GAAGGCGCGCTCGCCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354

Qy 973 GAAGGTGCTTACCATGTTCTTCCACAGGAGC 1003
Db 355 CCCCGCTGTNCCACNAGGTGTTCAACGAAC 385

RESULT 6
US-09-314-652
; Sequence 652, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670.314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060.756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 652
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-652

Query Match
Best Local Similarity 4.3%; Score 51.2; DB 4; Length 402;
Matches 152; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 673 AAAGTGCTCAACCTTGCTGCCAACTTGTCCCTCGGGCCCATCGACTCCAGGCTGTC 732
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 733 TCTCGGATAGACAGAGGTGACATTTATTAAGTCAAGACCCCTGATCTGCCGGGACGG 792
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 115 TCTCGGACCTGAGGTGTCAGGCTTACAAACCCGACCCACTCGTGCACACGACGG 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 793 CTGAAGGTGCTCGGCATCCAACTGCTGAATGCCGTCTCACGGTGGAGCGCCCTC 852
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 175 GTTCGGCCGGGATGGCCGGCGCTGCTGCANGTGGCGGAGACCATGCCCGCGGANCA 234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 853 CCCAAGTGACTGTGCCCTTCTCTGCTGCCAGGCTTCCGATCGCCTATGTGACAGC 912
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 235 CCGGATTGACCGCGCGCTGCTAGTGTGTCACGGCACCGGCTGATCCCATC 294
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 913 AAAGGGCTACCTGCTCATGGAGTAGCAAGACCGAGCAAGACTCTCAAGATTAT 972
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 295 GAAGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 973 GAAGTGCTACCTGCTTCTCCAAAGGAGC 1003
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 355 CCCCGGCTGTCACNAGGTGTTCAACGAAC 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-902-540-1131
; Sequence 1131, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1131
; LENGTH: 15572
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1131

Query Match
Best Local Similarity 4.1%; Score 48.4; DB 4; Length 15572;
Matches 162; Conservative 0; Mismatches 171; Indels 1; Gaps 1;

Qy 670 GCGAAAGTGCTCAACCTTGCTGCTCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTG 729
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10115 GCGAAGATGCTGGCAGCAATTTCTCCCGGGTGTCCCGGCGAGGACTGGACAGCAGATG 10174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 730 CTCTCTCGGAATAAGACAGAGGTGACATTTTATACTCAGACCCCTGATCTGCCGGGCA 789
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10175 TTCCTGACGACGCGCGGAGAGGCGGTTCCTCGGGATCGCTCATCACCCACG-A 10233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 790 GGGCTGAAGGTGCTCTTGGGATCCAACTGCTGAATGCGGTCTCACGGTGGAGCGGCC 849
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10234 GAGTGGCCGCGCGCTCCGCCAAGCGCTCATCCGCCCATCGAAGCGCTCGAGGGGAGG 10293
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 850 CTCCCCAAGCTGACTGTGCCCTTCTCTGCTCCAGGGCTCTGCCGATCGCTATGTGAC 909
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10294 CTCAGGACCTTGAGACTCCCTCTGCTGGTGTGACGGGGCGGAGGAGTTCATCCTCC 10353
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 910 AGCAAAAGGGGCTACCTGCTCATGGAGTTAGCCAAAGAGCCAGGACAAGACTTCTCAAGATT 969
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10354 ATCGAAGGCGAGCGCGCCCTGCTGGCGAGTCCACGATCGCGACAAGCGCTCATCATC 10413
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 970 TATGAAGGTGCTTACCATGTTCTCCACAAGAGC 1003
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 10414 TACGAGGGCCAGCGCCACGATCTCGCGCACGAAC 10447
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-252-991A-5873/c
; Sequence 5873, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5873
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5873

Query Match
Best Local Similarity 3.6%; Score 43.4; DB 4; Length 534;
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 387 CTGCTGCTGTTGCCCCACGACCATGTTGCCACGACAGCGAAGGGGAGAGATGCT 446
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 404 CTTCCAGCGCGTGGCGCGGACGCTCGGCTTTGCGCAGGGCGCGGAGAAACGCGGT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 447 AGTGTCTGACTTCCACGTTTTTCGTACGGGATGTTGTCAGCATGTGATTCATGCGAA 506
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 344 CGGCGCTGGCTCGACCTTCGCCAACGGCACCTGGTAGGTTTGAACGACCCGTAGCGGA 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 507 AGACTACCTCGGGCTTCTGTTCTTCCTTC 535
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 284 AGCTTCTGCTGGGCATCATCCCTTCCTGC 256
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-252-991A-5829/c
; Sequence 5829, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 5829  
; LENGTH: 1968  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5829

Query Match 3.6%; Score 43.4; DB 4; Length 1968;  
Best Local Similarity 55.7%; Pred. No. 0.055;  
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 387 CCTGCTGGTTCGCCACGACCATGTTGGCCAGGACAGCGAAGGGGAGGATGGT 446  
DB 1879 CCTCAGCGCGTCCCGGAGCAGCGTGGCCCTTTCGCGAGGCGCGGAGAAACGCGAGT 1820  
QY 447 AGTGTCTGACTTCCACGCTTTTCGTCAGGGATGTTGCGACATGCGATTCCATGCAGAA 506  
DB 1819 CGGCGTGGCTCGACCTTCGCCAACGCGACCTGGTAGTCTTGAAACGCGACCGTAGCGGA 1760  
QY 507 AGACTACCTGGGCTTCCTGTCTTCCTTC 535  
DB 1759 AGCCTCGCTGGGCATCATCCTTCCTGC 1731

## RESULT 10

US-09-252-991A-5779  
; Sequence 5779, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR APPLICATION NUMBER: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5779  
; LENGTH: 2190  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5779

Query Match 3.6%; Score 43.4; DB 4; Length 2190;  
Best Local Similarity 55.7%; Pred. No. 0.058;  
Matches 83; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 387 CCTGCTGGTTCGCCACGACCATGTTGGCCAGGACAGCGAAGGGGAGGATGGT 446  
DB 93 CCTCAGCGCGTCCCGGAGCAGCTGGCCCTTTCGCGAGGCGCGGAGAAACGCGAGT 152  
QY 447 AGTGTCTGACTTCCACGCTTTTCGTCAGGGATGTTGCGACATGCGATTCCATGCAGAA 506  
DB 153 CGGCGTGGCTCGACCTTCGCCAACGCGACCTGGTAGTCTTGAAACGCGACCGTAGCGGA 212  
QY 507 AGACTACCTGGGCTTCCTGTCTTCCTTC 535  
DB 213 AGCCTCGCTGGGCATCATCCTTCCTGC 241

## RESULT 11

US-09-621-976-2813/c  
; Sequence 2813, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 2813  
; LENGTH: 832  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 235..399  
US-09-621-976-2813

Query Match 3.3%; Score 39; DB 4; Length 832;  
Best Local Similarity 8.9%; Pred. No. 0.65;  
Matches 24; Conservative 135; Mismatches 110; Indels 0; Gaps 0;

QY 810 CATCCAACTCTCTCAATGCCCTCTCACGGGTGGAGCGGCCCTCCCCAAGCTGATGTGCC 869  
DB 290 CMYRGRRCAWYTWARGHMSYAWGKWSMSAMCTRMYYKGGSTYWTMKCTCATWCYW 231  
QY 870 CTTCTCTGCTCCAGGGCTCTCGCATCGCTATGTGACGAGCAAAAGGGGCTACCTGCT 929  
DB 230 YKWKWKMWSKTCWSGSGYMTSYSTRSYMYWASWMTMCWWGRWHSYHYMANGK 171  
QY 930 CATGGAGTTAGCCAAAGAGCCAGCAAGACTCTCAAGATTTATGAAGTGCCTTACCATGT 989  
DB 170 KWRYYATTWRRAMWWAAWMTWMMWAWCMSSRGAAMYRRRTMMWGYRYWNRKKSYYR 111  
QY 990 TCTCCAAAGGAGCTCTCGAAGTACCACCACTCGGTCTTCATGAAATAAATGATGTGGT 1049  
DB 110 TRCAWAYANKTKSYWCRWKRKRCMMMMMAVYKTMWRACWKTTRYRWMAWAMWR 51  
QY 1050 CTCTCAAGAGACAGCCAGCGCAAGAACTG 1078  
DB 50 MWWTMMMYTWYWRAMKRRWNRKWSWS 22

## RESULT 12

US-09-280-116-63/c  
; Sequence 63, Application US/09280116A  
; Patent No. 6331427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24. 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 865  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: trypsin-like serine proteases  
US-09-280-116-63

Query Match 3.3%; Score 39; DB 3; Length 865;  
Best Local Similarity 46.8%; Pred. No. 0.66;  
Matches 123; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 310 CTCATCTTTTGTGTCCTATGGAGCGGAGAGACAGATGGCGCTATGAAGAGCTGGCTCGG 369  
DB 430 CTACTCTCAGTTTGAGCTGAGCAAGGAAAACAGTGGCGCCGACACCTTGACTTGGCGCAG 371  
QY 370 ATGCTGATGGGCTGGACCTGCTGGTGTTCGCCACAGCATGTTGCCACGCGACAGAC 429  
DB 370 AACCTGGAGGCCCGCTGATGTCGTATCGAGAAATGCCAAAAACAGAAACAGAAAAAGC 311  
QY 430 GAAGGGGAGGAGTAGTGTCTGACTTCCAGTTCCTCAGGGATGTTGTCAGCAT 489  
DB 310 CACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTTCAGCCGAAATTTTGGGGAGGTG 251



Search completed: August 14, 2005, 06:04:02  
Job time : 254 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 03:13:18 ; Search time 791 Seconds  
(without alignments)  
9777.320 Million cell updates/sec

Title: U67963

Perfect score: 1192

Sequence: 1 CCAGCCCAAGGCGAGGTC.....CAAAAAAAAAAAAAAAAA 1192

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 324468913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10J\_NEW\_PUB.seq\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1192	100.0	1192	9	US-09-880-107-3409
2	1192	100.0	1192	16	Sequence 3409, Ap
3	1192	100.0	1192	17	Sequence 7, Appli
4	1192	100.0	1192	17	Sequence 17, Appl
5	1192	100.0	1192	17	Sequence 17, Appl
6	1192	100.0	1192	19	US-10-647-426-15
7	1192	100.0	1192	19	US-10-775-169-231

8	1192	100.0	1582	21	US-10-956-157-1759
9	1162	97.5	4193	16	US-10-240-965-141
10	1002	84.1	1309	21	US-10-498-788-49
11	942	79.0	942	16	US-10-303-664A-8
12	791.8	66.4	895	17	US-10-093-463-175
13	749	62.8	861	17	US-10-093-463-177
14	749	62.8	861	17	US-10-099-322-321
15	667.2	56.0	912	21	US-10-764-420-209
16	588	49.3	600	21	US-10-956-157-6994
17	519.8	43.6	556	10	US-09-918-995-29218
18	474.6	39.8	681	21	US-10-764-420-136
19	417	35.0	452	10	US-09-918-995-32498
20	364.8	30.6	425	10	US-09-918-995-7833
21	306.4	25.7	463	10	US-09-918-995-23507
22	210.6	17.7	501	10	US-09-918-995-10625
23	204.2	16.8	376	9	US-09-728-445-419
24	200	16.8	243	11	US-09-969-034-4029
25	198.4	16.6	506	9	US-09-917-800A-696
26	116.2	9.7	837	17	US-10-282-122A-28443
27	116.2	9.7	972	17	US-10-282-122A-28166
28	113	9.5	831	17	US-10-282-122A-25663
29	94.4	7.9	644	13	US-10-027-632-114757
30	94.4	7.9	644	17	US-10-027-632-114757
31	84.8	7.1	825	17	US-10-369-493-28150
32	84.8	7.1	825	17	US-10-369-493-30910
33	84.8	7.1	825	17	US-10-282-122A-13068
34	80.8	6.8	1590	20	US-10-739-930-2161
35	75.8	6.4	928	20	US-10-425-115-74280
36	74.8	6.3	1665	18	US-10-425-114-14081
37	74.8	6.3	2637	20	US-10-425-115-101074
38	71.4	6.0	840	17	US-10-282-122A-27862
39	70.8	5.9	946	19	US-10-437-963-97729
40	70.4	5.9	2619	20	US-10-357-930-23110
41	70.4	5.9	2619	20	US-10-357-930-28980
42	68.4	5.7	673	19	US-10-767-701-29426
43	66.2	5.6	909	17	US-10-282-122A-14592
44	65.6	5.5	927	17	US-10-369-493-24361
45	65	5.5	1476	20	US-10-425-115-128760

ALIGNMENTS

RESULT 1  
US-09-880-107-3409  
; Sequence 3409, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3409  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U67963  
US-09-880-107-3409

Query Match 100.0%; Score 1192; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 CCAGCCGAAAGGAGGAGGCTCGGGTCGGGAAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60  
Db 1 CCAGCCGAAAGGAGGAGGCTCGGGTCGGGAAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60  
Qy 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTCCTGGTTCCTGATTTCTCCAGGCTGTC 120  
Db 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTCCTGGTTCCTGATTTCTCCAGGCTGTC 120  
Qy 121 GTGGTTGTGGAATCAAAAGCCAGACATATAATGGAACAGGACCTGAAGACCTTCCAGC 180  
Db 121 GTGGTTGTGGAATCAAAAGCCAGACATATAATGGAACAGGACCTGAAGACCTTCCAGC 180  
Qy 181 ATGCCAGAGAAAGTTCCGCCAGGAGACCCCGAGAGCATTCCTTACAGGACCTCCCT 240  
Db 181 ATGCCAGAGAAAGTTCCGCCAGGAGACCCCGAGAGCATTCCTTACAGGACCTCCCT 240  
Qy 241 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCAAGTACTGGAACCCACAGGCACA 300  
Db 241 CACCTGGTCAATGACAGCGGACAGTACCTCTTCTGCAAGTACTGGAACCCACAGGCACA 300  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGAGAGCACAGTGGCGGCTATGAAG 360  
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGAGAGCACAGTGGCGGCTATGAAG 360  
Qy 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 421 GGACAGAGCAAGGAGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480  
Db 421 GGACAGAGCAAGGAGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480  
Qy 481 TTGCAGCATGTGGATTCATGACAGAAAGATCAACCTGGGCTCTGCTTCTTCTTCTGGGC 540  
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Qy 541 CACTCCATGGAGGCGCATCGCCATCTCTGCAAGTCTGCAAGTCTGCAAGTCTGCAAGTCT 600  
Db 541 CACTCCATGGAGGCGCATCGCCATCTCTGCAAGTCTGCAAGTCTGCAAGTCTGCAAGTCT 600  
Qy 601 GGCATGTACTCATTTGCGCTCTGCTTCTGCGCAATCTGCAAGTCTGCAAGTCTGCAAGTCT 660  
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Qy 661 GTCCTTGTGCGAAAGTGTCAACCTTTGTGTCGCAAACTTTGTCCTCGGCGCCATCGAC 720  
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Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTTCGACATTTATATACTCAGACCCCTGATC 780  
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Qy 781 TCCGCGGCGAGGCTGAAGGTGTGCTTCGCAATCAAACTGCTGAATGCGCTCTACAGGCTG 840  
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Qy 841 GAGCGCGCTTCCCAAGTGTGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 GAGCGCGCTTCCCAAGTGTGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 CTATGTGACAGCAAGGGGCTACTCTCATGAGTTAGCCAGAGGACGAGCAAGACT 960  
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Qy 961 CTCGAAGTTATGAAGTGTGCTACCATGTTCTCAACAGGAGCTTCTGTAAGTCAACCAAC 1020  
Db 961 CTCGAAGTTATGAAGTGTGCTACCATGTTCTCAACAGGAGCTTCTGTAAGTCAACCAAC 1020  
Qy 1021 TCCGCTTTCATGAATAAATGTGGTCTCTCAAGAGGACAGCCACGCGAGGAATCTGCG 1080  
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Qy 1081 TCCCAACCCCTGAATGATTCGCGGCTCGCGGCTCATGCTCTGGGGATGCGAGCAGGG 1140  
Db 1081 TCCCAACCCCTGAATGATTCGCGGCTCGCGGCTCATGCTCTGGGGATGCGAGCAGGG 1140  
Qy 1141 AAGGCGAGAGATGCTTCTCAGATATGCTTTCAGAAAAAAGAAAAA 1192  
Db 1141 AAGGCGAGAGATGCTTCTCAGATATGCTTTCAGAAAAAAGAAAAA 1192

RESULT 2  
US-10-303-664A-7  
; Sequence 7, Application US/10303664A  
; Publication No. US20030153018A1  
; GENERAL INFORMATION:  
; APPLICANT: Hunter, John Joseph  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Tsai, Fong-Ying  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,  
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,  
; TITLE OF INVENTION: 33794, 54476 and 94710  
; FILE REFERENCE: MPI2001-290P3R(M)  
; CURRENT APPLICATION NUMBER: US/10/303,664A  
; CURRENT FILING DATE: 2002-11-25  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (151) ... (1092)

US-10-303-664A-7

Query Match 100.0%; Score 1192; DB 16; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCGAAAGGAGGAGGCTCGGGTCGGGAAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60  
Db 1 CCAGCCGAAAGGAGGAGGCTCGGGTCGGGAAAGAGGGCTCGGAGCTGCTTCCTGCTGCC 60  
Qy 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTCCTGGTTCCTGATTTCTCCAGGCTGTC 120  
Db 61 TTGGGGCGCCGAGATGAGGAAACAGCCCGATTTCCTGGTTCCTGATTTCTCCAGGCTGTC 120  
Qy 121 GTGGTTGTGGAATGCAAAAGCCAGACATATAATGGAACAGGACCTGAAGACCTTCCAGC 180  
Db 121 GTGGTTGTGGAATGCAAAAGCCAGACATATAATGGAACAGGACCTTCCAGC 180  
Qy 181 ATGCCAGAGAAAGTTCCGCCAGGAGACCCCGAGAGCATTCCTTACAGGACCTCCCT 240  
Db 181 ATGCCAGAGAAAGTTCCGCCAGGAGACCCCGAGAGCATTCCTTACAGGACCTCCCT 240  
Qy 241 CACTGGTCAATGACAGCGGACAGTACCTCTTCTGCAAGTACTGGAACCCACAGGCACA 300  
Db 241 CACTGGTCAATGACAGCGGACAGTACCTCTTCTGCAAGTACTGGAACCCACAGGCACA 300  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGAGAGCACAGTGGCGGCTATGAAG 360  
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCCGAGAGCACAGTGGCGGCTATGAAG 360  
Qy 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 CTGGCTCGGATGCTGATGGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 421 GGACAGAGCAAGGAGAGAGTGGTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480  
Db 421 GGACAGAGCAAGGAGAGAGTGGTAGTGTCTGACTTCCACGTTTTCGTGAGGAGTGTG 480





;; TITLE OF INVENTION: A METHOD OF DETERMINING TUMOR CHARACTERISTICS BY  
;; TITLE OF INVENTION: DETERMINING ABNORMAL COPY NUMBER OR EXPRESSION LEVEL OF  
;; TITLE OF INVENTION: LIPID-ASSOCIATED GENES  
;; FILE REFERENCE: PATRICK EAGLEMAN: EMBOL-X 252/124  
;; CURRENT APPLICATION NUMBER: US/10/647,426  
;; CURRENT FILING DATE: 2003-08-26  
;; PRIOR APPLICATION NUMBER: US/09/676,052  
;; PRIOR FILING DATE: 2000-09-28  
;; NUMBER OF SEQ ID NOS: 95  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 15  
;; LENGTH: 1192  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: gene  
;; LOCATION: (1) .. (1192)  
;; OTHER INFORMATION: The sequence of the cDNA coding for Human  
;; OTHER INFORMATION: Lysophospholipase Homolog  
US-10-647-426-15

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCCTTCTCTGCTGCC 60

Qy 61 TTGGGGCGGCCAGATGAGGAAACAGCCGATTTGGCTGGTTCGTGATTTCCAGGCTGTC 120  
Db 61 TTGGGGCGGCCAGATGAGGAAACAGCCGATTTGGCTGGTTCGTGATTTCCAGGCTGTC 120

Qy 121 GTGGTGTGGAATGCACACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180  
Db 121 GTGGTGTGGAATGCACACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240  
Db 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240

Qy 241 CACCTGTCTAATGACAGGAGCAGTACTCTTCTGCGAGGTACTGGAACCCACAGGCACA 300  
Db 241 CACCTGTCTAATGACAGGAGCAGTACTCTTCTGCGAGGTACTGGAACCCACAGGCACA 300

Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGAGCCGAGAGCACGTGCGCTATGAAGAG 360  
Db 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGAGCCGAGAGCACGTGCGCTATGAAGAG 360

Qy 361 CTGGCTCGGATGTGATGGGCTGGACCTGCTGCTGTTTCCGCCACGACCATTTGGCCAC 420  
Db 361 CTGGCTCGGATGTGATGGGCTGGACCTGCTGCTGTTTCCGCCACGACCATTTGGCCAC 420

Qy 421 GGAAGAGCGAAGGGGAGAGATGTTGTTGCTGACCTTCCAGTTTTCGTGAGGATGTG 480  
Db 421 GGAAGAGCGAAGGGGAGAGATGTTGTTGCTGACCTTCCAGTTTTCGTGAGGATGTG 480

Qy 481 TTGAGCATGTGATTTCCATGCAAGAGACTACCTTGGGCTTCTGTTCTTCTTCTGGC 540  
Db 481 TTGAGCATGTGATTTCCATGCAAGAGACTACCTTGGGCTTCTGTTCTTCTTCTGGC 540

Qy 541 CACTTCCATGGAGGCGCATCGCCATCTCTACGCGCGCAGAGAGCGCGGCGCACTTCGCC 600  
Db 541 CACTTCCATGGAGGCGCATCGCCATCTCTACGCGCGCAGAGAGCGCGGCGCACTTCGCC 600

Qy 601 GGCATGTACTCATTTTCCGCTCTGGTCTTGGCCAACTCTGAATCTGCAACAACTTTCAAG 660  
Db 601 GGCATGTACTCATTTTCCGCTCTGGTCTTGGCCAACTCTGAATCTGCAACAACTTTCAAG 660

Qy 661 GTCCTTCTGCGAAAGTCTCAACTTGTGCTGCGCAAACTTGTCTCGGCGCCATCGAC 720  
Db 661 GTCCTTCTGCGAAAGTCTCAACTTGTGCTGCGCAAACTTGTCTCGGCGCCATCGAC 720

Qy 721 TCCAGCGTCTCTCTCGAATAAGACAGAGGTGACATTTATTAACCTCAGACCCCTGATC 780  
Db 721 TCCAGCGTCTCTCTCGAATAAGACAGAGGTGACATTTATTAACCTCAGACCCCTGATC 780

Qy 781 TGGCGGCGAGGCTGAGGTGCTTTCGGCATCCAACTGCTGAATGCCCTCTCAGCGGTG 840  
Db 781 TGGCGGCGAGGCTGAGAGGTGCTTTCGGCATCCAACTGCTGAATGCCCTCTCAGCGGTG 840

Qy 841 GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTCTGCTGCTCCAGGCTCTTCCGATCGC 900  
Db 841 GAGCGCGCCCTCCCAAGCTGACTGTGCCCTTCTCTGCTGCTCCAGGCTCTTCCGATCGC 900

Qy 901 CTATGTGACAGCAAAAGGCGCTACCTGCTCATGAGTTAGCCAAAGAGCCAGGACAAGACT 960  
Db 901 CTATGTGACAGCAAAAGGCGCTACCTGCTCATGAGTTAGCCAAAGAGCCAGGACAAGACT 960

Qy 961 CTCAAGATTTATGAAGTGCCTACCATGTTTCTCCAAAGAGGCTTCTGAGTCAACCAAC 1020  
Db 961 CTCAAGATTTATGAAGTGCCTACCATGTTTCTCCAAAGAGGCTTCTGAGTCAACCAAC 1020

Qy 1021 TCCGCTCTTCCATGAAATAAATCATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080  
Db 1021 TCCGCTCTTCCATGAAATAAATCATGTGGTCTCTCAAAAGGACAGCCAGGAGAACTGCG 1080

Qy 1081 TCCCAACCTTGAATGCAATGCGCGGTGCCCGGTCTCATGGTCTGGGGGATGCGAGGAG 1140  
Db 1081 TCCCAACCTTGAATGCAATGCGCGGTGCCCGGTCTCATGGTCTGGGGGATGCGAGGAG 1140

Qy 1141 AAGGCGAGAGTGGCTTCTCAGATATGGCTTGCAAAAAAANAANAANAANA 1192  
Db 1141 AAGGCGAGAGTGGCTTCTCAGATATGGCTTGCAAAAAAANAANAANAANA 1192

RESULT 6  
US-10-775-169-231  
; Sequence 231, Application US/10775169  
; Publication No. US20040175743A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dorner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
; FILE REFERENCE: AM101080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 231  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-169-231

Query Match 100.0%; Score 1192; DB 19; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCCTTCTCTGCTGCC 60  
Db 1 CCAGCCCGAAGGCGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTGCCTTCTCTGCTGCC 60

Qy 61 TTGGGGCGGCCAGATGAGGAAACAGCCGATTTGGCTGGTTCGTGATTTCCAGGCTGTC 120  
Db 61 TTGGGGCGGCCAGATGAGGAAACAGCCGATTTGGCTGGTTCGTGATTTCCAGGCTGTC 120

Qy 121 GTGGTGTGGAATGCACACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180  
Db 121 GTGGTGTGGAATGCACACGCCACATATGAAACAGAGCTGAAGACCTTCCAGC 180

Qy 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240  
Db 181 ATGCCAGAGAAAGTTCCCCCAGGCGGACCCCGAGAGCATTTCCCTACAGGACCTCCCT 240

181 ATGCCAGAGAAAGTTCCCCAGGCGGACCCCGCAGAGCAATTCCCTACCAAGCACTCCCT 240  
241 CACCTGGTCAATGACAGCGGACAGTACTCTTCTGCAGGTACTGGAACCCACAGGCACA 300  
241 CACCTGGTCAATGACAGCGGACAGTACTCTTCTGCAGGTACTGGAACCCACAGGCACA 300  
301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGAGACAGTGGCCGCTATGAAGAG 360  
301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGAGACAGTGGCCGCTATGAAGAG 360  
361 CTGCTCGGATGCTGATGGGCTCGAATCTGCTGGTGTTCGCCACGACCAATGTTGGCCAC 420  
361 CTGCTCGGATGCTGATGGGCTCGAATCTGCTGGTGTTCGCCACGACCAATGTTGGCCAC 420  
421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACCTTCCAGCTTTTCGTACGGGATGTG 480  
421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACCTTCCAGCTTTTCGTACGGGATGTG 480  
481 TTGAGAGATGTGGATTCATGCAGAAAGACTTACCCTGGGCTTCTGCTTCTTCTGGGC 540  
481 TTGAGAGATGTGGATTCATGCAGAAAGACTTACCCTGGGCTTCTGCTTCTTCTGGGC 540  
541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCCGGGCCACTTCGCC 600  
541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCCGGGCCACTTCGCC 600  
601 GGCATGCTACTCATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
601 GGCATGCTACTCATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
661 GTCTCTGCTGCGAAAGTCTCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
661 GTCTCTGCTGCGAAAGTCTCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
721 TCCAGCGTCTCTTCGGAATAAGACAGAGTGCACATTTATATACTCAGACCCCTGATC 780  
721 TCCAGCGTCTCTTCGGAATAAGACAGAGTGCACATTTATATACTCAGACCCCTGATC 780  
781 TGCCGCGAGCGCTGAGGTGTGCTTGGGCAATCCAACTGCTGANTGCGCTCAGCGGTG 840  
781 TGCCGCGAGCGCTGAGGTGTGCTTGGGCAATCCAACTGCTGANTGCGCTCAGCGGTG 840  
841 GAGCGCGCTTCCCAAGCTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
841 GAGCGCGCTTCCCAAGCTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
901 CTATGTGACAGAAAGGGGCTACTGCTCATGAGTTAGCCAGAGCCAGCAAGACT 960  
901 CTATGTGACAGAAAGGGGCTACTGCTCATGAGTTAGCCAGAGCCAGCAAGACT 960  
961 CTCAGATTTATGAAGTGTCTACCATGTTCTCCACAGGAGCTTCTGAGTCAACCAAC 1020  
961 CTCAGATTTATGAAGTGTCTACCATGTTCTCCACAGGAGCTTCTGAGTCAACCAAC 1020  
1021 TCCGCTTTCATGAAATAAATGAGGTCTCTCAAGAGCAGCCACGAGGAATCTGCG 1080  
1021 TCCGCTTTCATGAAATAAATGAGGTCTCTCAAGAGCAGCCACGAGGAATCTGCG 1080  
1081 TCCCCACCTGAAATGCAATGGCCGGTCCCGGCTCATGGTCTGGGGATGACAGCAGGG 1140  
1081 TCCCCACCTGAAATGCAATGGCCGGTCCCGGCTCATGGTCTGGGGATGACAGCAGGG 1140  
1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAA 1192  
1141 AAGGGCAGAGATGGCTTCTCAGATATGGCTTGCAGAAAAA 1192

RESULT 7  
US-10-755-889-673  
; Sequence 673 Application US/10755889  
; Publication No. US20040171823A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB  
; TITLE OF INVENTION: PATHWAY  
; FILE REFERENCE: D0284 NP  
; CURRENT APPLICATION NUMBER: US/10755,889  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: U.S. 60/440,068  
; PRIOR FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: U.S. 60/469,757  
; PRIOR FILING DATE: 2003-05-12  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 673  
; LENGTH: 1582  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-755-889-673

Query Match 100.0%; Score 1192; DB 19; Length 1582;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCGAAAGGCAGGGTCTGGGTGCGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC 60  
Db |||||  
379 CCAGCCGAAAGGCAGGGTCTGGGTGCGGAAGAGGCTCGAGCTGCTTCTCTGCTGCC 438  
Qy 61 TTGGGCGCGCCAGATGAGGGAACAGCCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db |||||  
439 TTGGGCGCGCCAGATGAGGGAACAGCCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498  
Qy 121 GTGCTTGTGAATGCAAAACGCGACACATATGAAACAGGACCTGAAGACCTTCCAGC 180  
Db |||||  
499 GTGCTTGTGAATGCAAAACGCGACACATATGAAACAGGACCTGAAGACCTTCCAGC 558  
Qy 181 ATGCCAGAGAAAGTTCCCGCAGCGGACCCCGCAGAGCAATTCCTTACCAGGACTCCCT 240  
Db |||||  
559 ATGCCAGAGAAAGTTCCCGCAGCGGACCCCGCAGAGCAATTCCTTACCAGGACTCCCT 618  
Qy 241 CACTGTGCTCAATGACAGCGGACGACGACTCTCTCTGCAAGTACTGGAACCCACAGGCACA 300  
Db |||||  
619 CACTGTGCTCAATGACAGCGGACGACGACTCTCTCTGCAAGTACTGGAACCCACAGGCACA 678  
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTCATGGAGCCGAGAGCAGTGGCCGCTATGAAGAG 360  
Db |||||  
679 CCCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGAGAGCAGTGGCCGCTATGAAGAG 738  
Qy 361 CTGGCTCGATGCTGATGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db |||||  
739 CTGGCTCGATGCTGATGGGCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798  
Qy 421 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTACGGGATGTG 480  
Db |||||  
799 GGACAGAGCGAAGGGGAGAGATGGTAGTGTCTGACTTCCACGTTTTCGTACGGGATGTG 858  
Qy 481 TTGAGAGATGTGGATTCATGTCGAAAGACTTACCTGGGCTTCTGCTTCTCTGCTGCC 540  
Db |||||  
859 TTGAGAGATGTGGATTCATGTCGAAAGACTTACCTGGGCTTCTGCTTCTCTGCTGCC 918  
Qy 541 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCCGGGCCACTTCGCC 600  
Db |||||  
919 CACTCCATGGAGCGCCATCGCCATCCTCAAGCCGCGAGAGAGCCGGGCCACTTCGCC 978  
Qy 601 GGATGCTACTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db |||||  
979 GGATGCTACTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038  
Qy 661 GTCTTCTGCGAAAGTCTCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db |||||  
1039 GTCTTCTGCGAAAGTCTCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098  
Qy 721 TCCAGCGTCTCTCTCGGAATAAGAGAGTGCACATTTATATACTCAGACCCCTGATC 780  
Db |||||  
1099 TCCAGCGTCTCTCTCGGAATAAGAGAGTGCACATTTATATACTCAGACCCCTGATC 1158

Qy	781	TGCCGGGACAGGGCTGAAGGTGTGCTTTCGGCATCCAACTGCTGAATCCCGTCTCACGGGTG	840
Db	1159	TGCCGGGGCAGGGCTGAAGGTGTGCTTTCGGCATCCAACTGCTGAATGCCGTCTCACGGGTG	1218
Qy	841	GAGCGGCGCCTCCCAAGCTGACTGTGTGCCCTTCCTGTGCTCCAGGGCTCTGCCGATCGC	900
Db	1219	GAGCGGCGCCTCCCAAGCTGACTGTGTGCCCTTCCTGTGCTCCAGGGCTCTGCCGATCGC	1278
Qy	901	CTATGTGACAGCAAAAGGGCCCTACCTGTCTCATGTAGGTTAGCCAAAGACGACGAAGAAGT	960
Db	1279	CTATGTGACAGCAAAAGGGCCCTACCTGTCTCATGTAGGTTAGCCAAAGACGACGAAGAAGT	1338
Qy	961	CTCAAGATTTATGAAGTGCCCTACCATGTTCTCCACAGGAGCTTCCTGAAGTCAACCAAC	1020
Db	1339	CTCAAGATTTATGAAGTGCCCTACCATGTTCTCCACAGGAGCTTCCTGAAGTCAACCAAC	1398
Qy	1021	TCCGTCTTCCATGAAATAAAACATGTGGTGCTCTCAAAGACAGCCACGGCAGGAAGTGGC	108
Db	1399	TCCGTCTTCCATGAAATAAAACATGTGGTGCTCTCAAAGACAGCCACGGCAGGAAGTGGC	1458
Qy	1081	TCCCCACCCTGAATGCATGTGGCGGTGCCCGGCTCATGGTCTGGGGGATGCAGGCAGGGG	1140
Db	1459	TCCCCACCCTGAATGCATGTGGCGGTGCCCGGCTCATGGTCTGGGGGATGCAGGCAGGGG	1518
Qy	1141	AAGGCGACAGATGGCTTCTCAGATATGCTTGCAAAAAAAAAAAAAAAAAAAAAA	1192
Db	1519	AAGGCGACAGATGGCTTCTCAGATATGCTTGCAAAAAAAAAAAAAAAAAAAAAA	1570
RESULT 8			
US-10-956-157-1759			
; Sequence 1759, Application US/10956157			
; Publication No. US20050118625A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William			
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCI			
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES			
; FILE REFERENCE: 031896-043000 (AM 101081)			
; CURRENT APPLICATION NUMBER: US/10/956,157			
; CURRENT FILING DATE: 2004-10-04			
; NUMBER OF SEQ ID NOS: 319805			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 1759			
; LENGTH: 1582			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-956-157-1759			

Qy	301	CCCAAGCCCTCATCTTTGTGTC	CCCATGGAGCCGGAGACACAGTGC	CCCTATGAAGAG	360
Db	679	CCCAAGCCCTCATCTTTGTGTC	CCCATGGAGCCGGAGACACAGTGC	CCCTATGAAGAG	738
Qy	361	CTGGCTCGGATGCTGATGGGGCTGGAC	CTGCTGGTGTTCGCCACGACCACTGTTGGCCAC	420	
Db	739	CTGGCTCGGATGCTGATGGGGCTGGAC	CTGCTGGTGTTCGCCACGACCACTGTTGGCCAC	798	
Qy	421	GGACAGAGCGAAGGGGAGAGGATGTGATGTCTGAC	TTTCCACGTTTTCGTCAGGGATGTG	480	
Db	799	GGACAGAGCGAAGGGGAGAGGATGTGATGTCTGAC	TTTCCACGTTTTCGTCAGGGATGTG	858	
Qy	481	TTGCAGCATGTGGATTCCATCGAAGAAC	CTACCCTGGGCTTCTGTCCTTCTCTTCGGGC	540	
Db	859	TTGCAGCATGTGGATTCCATCGAAGAAC	CTACCCTGGGCTTCTGTCCTTCTCTTCGGGC	918	
Qy	541	CACCTCATGGAGCGCCATCGCCATCCTCA	CGGCGCAGAGAGGCGGGGCCACTTCGCC	600	
Db	919	CACCTCATGGAGCGCGCATCGCCATCCTCA	CGGCGCAGAGAGGCGGGGCCACTTCGCC	978	
Qy	601	GGCATGTACTCATTTTCGCTCTGGTTC	TTGCGAACTCTGAACTGCAAACTTCAAG	660	
Db	979	GGCATGTACTCATTTTCGCTCTGGTTC	TTGCGAACTCTGAACTGCAAACTTCAAG	1038	
Qy	661	GTCCTTCTCGAAAGTGCTCAACTTTGTGCT	TGCGAACTTGTCCCTCGGGCCCATCGAC	720	
Db	1039	GTCCTTCTCGAAAGTGCTCAACTTTGTGCT	TGCGAACTTGTCCCTCGGGCCCATCGAC	1098	
Qy	721	TCGAGCGTGCTCTCGGAATAAGACAGAGGT	TGACATTTTAACTCAGAGCCCTTGATC	780	
Db	1099	TCCAGCGTGCTCTCTCGGAATAAGACAGAGGT	TGACATTTTAACTCAGAGCCCTTGATC	1158	
Qy	781	TGCCGGGCAGGGCTGAAGGTGTGCTTCGGCAT	CCAACTCGAATGCCTCTCACGGGTG	840	
Db	1159	TGCCGGGCAGGGCTGAAGGTGTGCTTCGGCAT	CCAACTCGAATGCCTCTCACGGGTG	1218	
Qy	841	GAGCGCCCTTCCCAAAGCTGACTGTGCCCTTCT	TGCTGCCAGGCTCTGCCGATCGC	900	
Db	1219	GAGCGCCCTTCCCAAAGCTGACTGTGCCCTTCT	TGCTGCCAGGCTCTGCCGATCGC	1278	
Qy	901	CTATGTACACAGCAAGGGGCTACCTGCTCAT	TGGAGTTAGCCAGAGCCAGGACAAGACT	960	
Db	1279	CTATGTACACAGCAAGGGGCTACCTGCTCAT	TGGAGTTAGCCAGAGCCAGGACAAGACT	1338	
Qy	961	CTCAAGATTTTGAAGTGCTTACCATTGTCTTCC	ACAAGGAGCTTCTGTAAGTCAACCAAC	1020	
Db	1339	CTCAAGATTTTGAAGTGCTTACCATTGTCTTCC	ACAAGGAGCTTCTGTAAGTCAACCAAC	1398	
Qy	1021	TCCGTCTTCATGAAATAAACA	TGTGGGTCTCTCAAAGGACAGCCACGGCAGGAACTGCG	1080	
Db	1399	TCCGTCTTCATGAAATAAACA	TGTGGGTCTCTCAAAGGACAGCCACGGCAGGAACTGCG	1458	
Qy	1081	TCCCCACCTCTGAATGCAATTCGGCGGTGCC	CGGCTCATGGTCTGGGGGATGCAGGCAGGGG	1140	
Db	1459	TCCCCACCTCTGAATGCAATTCGGCGGTGCC	CGGCTCATGGTCTGGGGGATGCAGGCAGGGG	1518	
Qy	1141	AAGGGCAGAGATGGCTTCTCAGATATATGGCT	TTGCAAAAAA	1192	
Db	1519	AAGGGCAGAGATGGCTTCTCAGATATATGGCT	TTGCAAAAAA	1570	

RESULT 9  
US-10-240-365-141  
; Sequence 141, Application US/10240965  
; Publication No. US2003016592A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN DOV.  
; APPLICANT: SOMOGHI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEITHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas



```
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ. ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 141
; LENGTH: 4193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 216063.17
; NAME/KEY: unsure
; LOCATION: 1626-1649
; OTHER INFORMATION: a, t, c, g, or other
US-10-240-965-141

Query Match          97.5%; Score 1162; DB 16; Length 4193;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCTGCTGCC 60
Db 452 CCAGCCGAAAGGACAGGGTCTGGGTGCGGGAAGAGGGCTCGGAGCTGCTTCTGCTGCC 511
Qy 61 TTGGGGCGCCGACATGAGGAAAGAGCCGATTTGCCCTGGTTCGATTTCTCAGGCTGTC 120
Db 512 TTGGGGCGCCGACATGAGGAAAGAGCCGATTTGCCCTGGTTCGATTTCTCAGGCTGTC 571
Qy 121 GTGGTTGTGGAATCAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 572 GTGGTTGTGGAATCAACGCCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 631
Qy 181 ATGCCAGAGGAAGTTCCGCCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 240
Db 632 ATGCCAGAGGAAGTTCCGCCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 691
Qy 241 CACTTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACT-GGAAACCCACAGGCAC 299
Db 692 CACTTGGTCAATGACAGCGGACAGTACCTCTTCTGCGAGTACTGGGAAACCCACAGGCAC 751
Qy 300 ACCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA 359
Db 752 ACCAAGGCCCTCATCTTTGTGTCCCATGGAGCCGGAGACACAGTGGCCGCTATGAAGA 811
Qy 360 GCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGTGTTCCGCCACGACATGTTGGCCA 419
Db 812 GCTGGCTCGGATGCTGATGGGGCTGGACCTGCTGTGTTCCGCCACGACATGTTGGCCA 871
Qy 420 CGGACAGACCAAGGGAGAGATGTTAGTCTGTGACTTCCACGTTTTCGTCAGGAGTGT 479
Db 872 CGGACAGACCAAGGGAGAGATGTTAGTCTGTGACTTCCACGTTTTCGTCAGGAGTGT 931
Qy 480 GTTGACGATGTGATTCATTCGACAGAAAGACTACCTGGGCTTCTGTCCTTCTTCTGGG 539
Db 932 GTTGACGATGTGATTCATTCGACAGAAAGACTACCTGGGCTTCTGTCCTTCTTCTGGG 991
Qy 540 CCATCTCATGGAGCGGCATCGCCATCTCAGCGCCGACAGAGGCGCGGCCCATCTTGC 599
Db 992 CCATCTCATGGAGCGGCATCGCCATCTCAGCGCCGACAGAGGCGCGGCCCATCTTGC 1051
Qy 600 CGGATGTGTACTCATTTTCGCTCTGTTCTTGGCAATCCTCAATCTGCAACAACCTTCAA 659
Db 1052 CGGATGTGTACTCATTTTCGCTCTGTTCTTGGCAATCCTCAATCTGCAACAACCTTCAA 1111
Qy 660 GGTCTTGTCTCGAAAGTGTCAACCTTGTGTGTCGCAAACTTGTCCCTCGGGCCCATCGA 719
Db 1112 GGTCTTGTCTCGAAAGTGTCAACCTTGTGTGTCGCAAACTTGTCCCTCGGGCCCATCGA 1171
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Qy 720 CTCGAGCGTCTCTCTCGGAATAAGACAGAGGTTCGACATTTATAACTCAGACCCCTGAT 779
Db 1172 CTCGAGCGTCTCTCTCGGAATAAGACAGAGGTTCGACATTTATAACTCAGACCCCTGAT 1231
Qy 780 CTGCGCGGCGAGGGCTGAAGGTGTGCTTTCCGATCCAACTGCTGAATGCCGCTCTCACGGGT 839
Db 1232 CTGCGCGGCGAGGGCTGAAGGTGTGCTTTCCGATCCAACTGCTGAATGCCGCTCTCACGGGT 1291
Qy 840 GGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTCTGCTCTCAGGGCTTGTCCGATCG 899
Db 1292 GGAGCGCGCCCTCCCCAAGCTGACTGTGCCCTTCTCTGCTCTCAGGGCTTGTCCGATCG 1351
Qy 900 CCTATGTGACAGCAAGGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCAGGACAGAC 959
Db 1352 CCTATGTGACAGCAAGGGGCTTACCTGCTCATGGAGTTAGCCAAAGAGCAGGACAGAC 1411
Qy 960 TCTCAAGATTATGAAGGTGCTTACCATGTTCTCCAAAGAGGCTTCTCTGAAGTCACCAA 1019
Db 1412 TCTCAAGATTATGAAGGTGCTTACCATGTTCTCCAAAGAGGCTTCTCTGAAGTCACCAA 1471
Qy 1020 CTCGCTCTTCCATGAATAAACAATGTGGGTCTCTCAAAGAGACGCCACGGCAGGAATGTC 1079
Db 1472 CTCGCTCTTCCATGAATAAACAATGTGGGTCTCTCAAAGAGACGCCACGGCAGGAATGTC 1531
Qy 1080 GTCCCCACCTCTGAATGCTTGGCCGGTGGCCGGCTCATGGTCTGGGGGATGCAGGCAGGG 1139
Db 1532 GTCCCCACCTCTGAATGCTTGGCCGGTGGCCGGCTCATGGTCTGGGGGATGCAGGCAGGG 1591
Qy 1140 GAAGGGCAGAGATGGCTTCTCAGATATGGCTTGC 1173
Db 1592 GAAGGGCAGAGATGGCTTCTCAGATATGGCTTGC 1625
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RESULT 10
US-10-498-788-49
; Sequence 49, Application US/10498788
; Publication No. US20050118594A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Narinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Lee, Ernestine A.
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Khare, Reena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Erika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April J. A.
; APPLICANT: Jin, Pei
; APPLICANT: Swarnakar, Anita
; APPLICANT: Li, Joana X.
; APPLICANT: Marquis, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; APPLICANT: Elliott, Vicki S.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1312 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/343,558
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/351,107
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; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PERL Program  
; SEQ ID NO 49  
; LENGTH: 1309  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7505864CB1  
US-10-498-788-49

Query Match 84.1%; Score 1002; DB 21; Length 1309;  
Best Local Similarity 92.4%; Pred. No. 2.1e-305;  
Matches 1102; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

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Qy 1 CCAGCCGAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTCGCTTCCTGCTGCC 60
Db 206 CCAGCCGAAGGAGGCTCTGGGTGCGGGAAGAGGCTCGAGCTCGCTTCCTGCTGCC 265
Qy 61 TTGGGGCCGCCAGATGAGGGAACAGCCGATTTGGCTTCTGATTTCTCCAGGCTGTC 120
Db 266 TTGGGGCCGCCAGATGAGGGAACAGCCGATTTGGCTTCTGATTTCTCCAGGCTGTC 325
Qy 121 GTGTTTGTGAATCAACCGCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 180
Db 326 GTGTTTGTGAATCAACCGCAGCACATATGGAACAGGACCTGAAGACCTTCCAGC 385
Qy 181 ATGCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 240
Db 386 ATGCAGAGGAAGTTCCCGCAGCGGACCCCGCAGAGCATTCCTTACAGGACCTCCCT 445
Qy 241 CACCTGTCAATGACAGCGACGACTTCTTCTGCAAGTACTGGAACCCACAGGACCA 300
Db 446 CACCTGTCAATGACAGCGACGACTTCTTCTGCAAGTACTGGAACCCACAGGACCA 505
Qy 301 CCCAAGGCCCTCATCTTTGTGTCCTAGGACCGGAGCAGACAGTGGCGCTATGAAG 360
Db 506 CCCAAGGCCCTCATCTTTGTGTCCTAGGACCGGAGCAGACAGTGGCGCTATGAAG 565
Qy 361 CTGCTCGGATGCTGATGGGCTGACCTGTGTGTGTCGCGCCAGACCATGTTGGCC 420
Db 566 CTGCTCGGATGCTGATGGGCTGACCTGTGTGTGTCGCGCCAGACCATGTTGGCC 625
Qy 421 GGACAGAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTGAGGATGT 480
Db 626 GGACAGAGCGAAGGGAGAGATGCTAGTGTCTGACTTCCACGTTTTCGTGAGGATGT 685
Qy 481 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCTTCTGGC 540
Db 686 TTGAGCATGTGGATTCATGCAGAAAGACTACCTGGGCTTCCTGCTTCTTCTGGC 745
Qy 541 CACTCCATGGAGCGGCATCGCCATCTCAGCGCGCAGAGAGCGCGGCGCACTTGGC 600
Db 746 CACTCCATGGAGCGGCATCGCCATCTCAGCGCGCAGAGAGCGCGGCGCACTTGGC 805
Qy 601 GGCATGCTACTCATTTGCGCTTCTGCTTCCCAATCTGCAATCTGCAACAACTTCAAG 660
Db 806 GGCATGCTACTCATTTGCGCTTCTGCTTCCCAATCTGCAATCTGCAACAACTTCAAG 863
Qy 661 GTCCTTGTGCGAAAGTGTCTCAACCTTGTGTGTCGCAAACTTGTCTCGGCGCCATCGAC 720
Db 864 ----- 863
Qy 721 TCCAGCGTGTCTCTCGGAATAAGACAGAGTTCGACATTTTAACTCAGACCCCTGATC 780
Db 864 -----AGTTCGACATTTTAACTCAGACCCCTGATC 895
Qy 781 TGGCGGCGAGGCTGAAGGTGTCTTGGGCATCCAACTGCTGAATGCGGCTCTCAGGGTG 840
Db 896 TGGCGGCGAGGCTGAAGGTGTCTTGGGCATCCAACTGCTGAATGCGGCTCTCAGGGTG 955
Qy 841 GAGGCGCGCCTCCCCAAGCTGACTGTGCTTCTGCTGCTCCAGGGCTCTGCGGATCGC 900
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Db 956 GAGCGCGCCTCCCAAGCTGACTGTGCCCTTCTGCTGCTCCAGGCTCTGCCGATCGC 1015
Qy 901 CTATGTGACAGCAAGGGCTTACCTGCTCATGAGTTAGCAGAGCCAGGACCAAGACT 960
Db 1016 CTATGTGACAGCAAGGGCTTACCTGCTCATGAGTTAGCAGAGCCAGGACCAAGACT 1075
Qy 961 CTCAGAATTTATGAAGTGTGCTTACCATGTTCTCCAAAGGAGCTTCTGAAGTCAACAA 1020
Db 1076 CTCAGAATTTATGAAGTGTGCTTACCATGTTCTCCAAAGGAGCTTCTGAAGTCAACAA 1135
Qy 1021 TCGTCTTTCATGAAATAAATGTTGGTCTCTCAAGGACAGCCAGGAGGACTGCG 1080
Db 1136 TCGTCTTTCATGAAATAAATGTTGGTCTCTCAAGGACAGCCAGGAGGAACTGCG 1195
Qy 1081 TCCCCACCTTGAATGCAATGCGCGGTGCCCGGCTCATGGTCTGGGGGATGCGAGCAGGG 1140
Db 1196 TCCCCACCTTGAATGCAATGCGCGGTGCCCGGCTCATGGTCTGGGGGATGCGAGCAGGG 1255
Qy 1141 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAGGAGGAGGAGG 1192
Db 1256 AAGGCGAGAGATGGCTTCTCAGATATGGCTTGCAAAAAAAGGAGGAGGAGGAGG 1307
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## RESULT 11

US-10-303-664A-8  
; Sequence 8, Application US/10303664A  
; Publication No. US20030153018A1  
; GENERAL INFORMATION:  
; APPLICANT: Hunter, John Joseph  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Teal, Fong-Ying  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609  
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,  
; TITLE OF INVENTION: 33794, 54476 and 94710  
; FILE REFERENCE: MPI2001-290P3R(M)  
; CURRENT APPLICATION NUMBER: US/10/303,664A  
; CURRENT FILING DATE: 2002-11-25  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 942  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-664A-8

Query Match 79.0%; Score 942; DB 16; Length 942;

Best Local Similarity 100.0%; Pred. No. 1.7e-286;

Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 151 ATGAAAACAGGACCTGAAGACCTTCCAGCATGCGAGGAAAGTTCCTCCAGCGGACC 210
Db 1 ATGAAAACAGGACCTGAAGACCTTCCAGCATGCGAGGAAAGTTCCTCCAGCGGACC 60
Qy 211 CCGCAGAGCATTCCTACCGAGCTCCCTCACCTGTCATGTCAGAGCAGGACAGTACCTC 270
Db 61 CCGCAGAGCATTCCTACCGAGCTCCCTCACCTGTCATGTCAGAGCAGGACAGTACCTC 120
Qy 271 TTCTGCGAGTACTGGAACCCACAGGACACCCAGGCCCTCATCTTTGTGTCATCGA 330
Db 121 TTCTGCGAGTACTGGAACCCACAGGACACCCAGGCCCTCATCTTTGTGTCATCGA 180
Qy 331 GCCGGAGAGCAGTGGCGCGCTATGAAGAGCTGCTCGGATGCTGATGGGCTGACCTG 390
Db 181 GCCGGAGAGCAGTGGCGCGCTATGAAGAGCTGCTCGGATGCTGATGGGCTGACCTG 240
Qy 391 CTGTGTGTCGCCACAGCACCATTGTTGGCCACGACAGAGCGAGGAGAGGATGTTAGT 450
Db 241 CTGTGTGTCGCCACAGCACCATTGTTGGCCACGACAGAGCGAGGAGGAGGATGTTAGT 300
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Qy	TCTGACTTCCACGTTTTCGTGAGGGATGTGTGACGATGTGGATTCATGACGAAAGAC	510
Db	TCTGACTTCCACGTTTTCGTGAGGGATGTGTGACGATGTGGATTCATGACGAAAGAC	360
Qy	TACCTGGGCTTCCTGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATGCCATCCTC	570
Db	TACCTGGGCTTCCTGTCTTCTTCTGGGCCACTCCATGGGAGGGCCCATGCCATCCTC	420
Qy	ACGGCCGACAGAGCGCCGGGCCACTTCGCCCGCATGGTACTCATTTTCGCCTCTGGTTCTT	630
Db	ACGGCCGACAGAGCGCCGGGCCACTTCGCCCGCATGGTACTCATTTTCGCCTCTGGTTCTT	480
Qy	GCCAACTCTGAACTCTGCAACAACATTTCAAGTCTCTGCTGGAAAGTCTCAACTCTGTG	690
Db	GCCAACTCTGAACTCTGCAACAACATTTCAAGTCTCTGCTGGAAAGTCTCAACTCTGTG	540
Qy	CTGCCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAAATAAGACAGAG	750
Db	CTGCCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAAATAAGACAGAG	600
Qy	GTCCACATTTATACTCAGACCCCTGATCTGCCGGGACAGGGCTGAAGGTGTCTTCGGC	810
Db	GTCCACATTTATACTCAGACCCCTGATCTGCCGGGACAGGGCTGAAGGTGTCTTCGGC	660
Qy	ATCCAACTGCTGAAATGCCGTCTCACGGTGGAGCGCCCTCCCCAAAGCTGACTGTGCC	870
Db	ATCCAACTGCTGAAATGCCGTCTCACGGTGGAGCGCCCTCCCCAAAGCTGACTGTGCC	720
Qy	TTCCTGTGCTCCAGGGCTCTGCCGATCGCCTATGTGACAGCAAGGGGCCCTACCTGCTC	930
Db	TTCCTGTGCTCCAGGGCTCTGCCGATCGCCTATGTGACAGCAAGGGGCCCTACCTGCTC	780
Qy	ATGAGTTTATGACAGAGCCAGACAGACTCTCAAGATTTATGAAGTGTGCTTACCATGTT	990
Db	ATGAGTTTATGACAGAGCCAGACAGACTCTCAAGATTTATGAAGTGTGCTTACCATGTT	840
Qy	CTCCACAAGGAGCTTCTTGAAGTCAACAATCCCGTCTTCCATGAAATAAAATGTGGGTC	1050
Db	CTCCACAAGGAGCTTCTTGAAGTCAACAATCCCGTCTTCCATGAAATAAAATGTGGGTC	900
Qy	TCTCAAAGGACAGCCACGGCAGGAATGTGCTGCCACCTCGA	1092
Db	TCTCAAAGGACAGCCACGGCAGGAATGTGCTGCCACCTCGA	942

RESULT 12

US-10-093-463-175  
; Sequence 175, Application US/10093463

; Publication No. US20030208039A1

GENERAL INFORMATION:	APPLICANT: Padigaru, Muralidhara
APPLICANT:	Shenoy, Suresh
APPLICANT:	Kusev, Ramesh
APPLICANT:	Gudea, Vladimir
APPLICANT:	Pochart, Pascal
APPLICANT:	Zhong, Mei
APPLICANT:	Rastelli, Luca
APPLICANT:	Mezas, Peter
APPLICANT:	Smithson, Glenda
APPLICANT:	Guo, Xiaojia
APPLICANT:	Gerlach, Valerie
APPLICANT:	Casman, Stacie
APPLICANT:	Boldog, Ferenc
APPLICANT:	Li, Li
APPLICANT:	Zernusen, Bryan
APPLICANT:	Tchernev, Velizar
APPLICANT:	Gangolli, Esha
APPLICANT:	Vernet, Corine
APPLICANT:	Pena, Carol
APPLICANT:	Burgess, Catherine
APPLICANT:	Liu, Xiaohong
APPLICANT:	Spytek, Kimberly
APPLICANT:	Gorman, Linda

```

1  APPLICANT: Spaderna, Steven
2  APPLICANT: Voss, Edward
3  APPLICANT: Malyankar, Uriel
4  APPLICANT: Anderson, David
5  APPLICANT: Pasturajan, Meera
6  APPLICANT: Miller, Charles
7  APPLICANT: Taupier, Raymond J. Jr.
8  TITLE OF INVENTION: No. US20030208039Allel Antibodies that Bind to Antigenic
9  TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
10 FILE REFERENCE: 21402-290A (Cura 590AT)
11 CURRENT APPLICATION NUMBER: US/10/093,463
12 CURRENT FILING DATE: 2002-06-24
13 PRIOR APPLICATION NUMBER: 60/278,675
14 PRIOR FILING DATE: 2001-04-14
15 PRIOR APPLICATION NUMBER: 60/338,092
16 PRIOR FILING DATE: 2001-12-03
17 PRIOR APPLICATION NUMBER: 60/274,281
18 PRIOR FILING DATE: 2001-03-08
19 PRIOR APPLICATION NUMBER: 60/274,101
20 PRIOR FILING DATE: 2001-03-08
21 PRIOR APPLICATION NUMBER: 60/325,681
22 PRIOR FILING DATE: 2001-09-27
23 PRIOR APPLICATION NUMBER: 60/304,354
24 PRIOR FILING DATE: 2001-07-10
25 PRIOR APPLICATION NUMBER: 60/279,995
26 PRIOR FILING DATE: 2001-03-30
27 PRIOR APPLICATION NUMBER: 60/294,899
28 PRIOR FILING DATE: 2001-05-31
29 PRIOR APPLICATION NUMBER: 60/287,424
30 PRIOR FILING DATE: 2001-04-30
31 PRIOR APPLICATION NUMBER: 60/299,027
32 PRIOR FILING DATE: 2001-06-18
33 PRIOR APPLICATION NUMBER: 60/309,198
34 PRIOR FILING DATE: 2001-07-31
35 PRIOR APPLICATION NUMBER: 60/281,194
36 PRIOR FILING DATE: 2001-04-04
37 PRIOR APPLICATION NUMBER: 60/274,194
38 PRIOR FILING DATE: 2001-03-08
39 PRIOR APPLICATION NUMBER: 60/274,849
40 PRIOR FILING DATE: 2001-03-09
41 PRIOR APPLICATION NUMBER: 60/330,380
42 PRIOR FILING DATE: 2001-10-18
43 PRIOR APPLICATION NUMBER: 60/275,235
44 PRIOR FILING DATE: 2001-03-12
45 PRIOR APPLICATION NUMBER: 60/288,342
46 PRIOR FILING DATE: 2001-05-03
47 PRIOR APPLICATION NUMBER: 60/275,578
48 PRIOR FILING DATE: 2001-03-13
49 NUMBER OF SEQ ID NOS: 370
50 SOFTWARE: PatentIn Ver. 2.1
51 SEQ ID NO 175
52 LENGTH: 895
53 TYPE: DNA
54 ORGANISM: Homo sapiens
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: (36)..(885)
58 US-10-091-463-175

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9



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Query Match      62.8%; Score 749; DB 17; Length 861;
Best Local Similarity 90.4%; Pred. No. 1.5e-225;
Matches 849; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 151 ATGGAACAGAGACCTTGAAGACCTTCCAGCATGCGAGGAAAGTTCCCCAGCGGACC 210
Db 7 ATGGAACAGAGACCTTGAAGACCTTCCAGCATGCGAGGAAAGTTCCCCAGCGGACC 66

Qy 211 CCGCAGAGCATTCCTACAGGACCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 270
Db 67 CCGCAGAGCATTCCTACAGGACCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 126

Qy 271 TTCTGCAGTACTGGAACCCACAGGACACCCAAAGGCCCTCATCTTGTGTCCCATGGA 330
Db 127 TTCTGCAGTACTGGAACCCACAGGACACCCAAAGGCCCTCATCTTGTGTCCCATGGA 186

Qy 331 GCCGAGAGCAGTGGCCGCTATGAAGAGCTGGCTCGATGCTGATGGGCTGAGCCTG 390
Db 187 GCCGAGAGCAGTGGCCGCTATGAAGAGCTGGCTCGATGCTGATGGGCTGAGCCTG 246

Qy 391 CTGGTGTTCGCCACGACCATGTTGGCCACGACAGCGGAAGGGAGAGGATGGTAGTG 450
Db 247 CTGGTGTTCGCCACGACCATGTTGGCCACGACAGCGGAAGGGAGAGGATGGTAGTG 306

Qy 451 TCTGACTTCCACGTTTTCGTGAGGATGTTGTCAGCATGTCGATGTCGAAAGTGCTCAACCTTTGTG 690
Db 307 TCTGACTTCCACGTTTTCGTGAGGATGTTGTCAGCATGTCGATGTCGAAAGTGCTCAACCTTTGTG 514

Qy 691 CTGCCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 750
Db 515 -----AG 516

Qy 751 GTCCACATTTATACTCAGACCCCTGATCTGCGGGGAGGGCTGAAGGTGTGCTTCGGC 810
Db 517 GTCCACATTTATACTCAGACCCCTGATCTGCGGGGAGGGCTGAAGGTGTGCTTCGGC 576

Qy 811 ATCCAACTGCTGAATGCGCTCTCAGGGTGGAGCGCGCCCTCCCAAGCTGACTGTGCC 870
Db 577 ATCCAACTGCTGAATGCGCTCTCAGGGTGGAGCGCGCCCTCCCAAGCTGACTGTGCC 636

Qy 871 TTCCTGCTCCAGGGCTTCGCGATGCGCTATGTGACAGCAAGAGGGGCTTACCTGCTC 930
Db 637 TTCCTGCTCCAGGGCTTCGCGATGCGCTATGTGACAGCAAGAGGGGCTTACCTGCTC 696

Qy 931 ATGGAGTTAGCCAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTACCATGTT 990
Db 697 ATGGAGTTAGCCAGAGCCAGGACAGACTCTCAAGATTTATGAAGTGCCTACCATGTT 756

Qy 991 CTCACAAAGAGGCTTCCTGAAAGTCAACAACTCCGTCTTCCATGAAATAAATATGTTGGT 1050
Db 757 CTCACAAAGAGGCTTCCTGAAAGTCAACAACTCCGTCTTCCATGAAATAAATATGTTGGT 816

Qy 1051 TCTCAAAGGACAGCCAGCGGACAGTGGTCCCAACC 1089
Db 817 TCTCAAAGGACAGCCAGCGGACAGTGGTCCCAACC 855
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RESULT 14

US-10-099-322-321  
; Sequence 321, Application US/10099322  
; Publication No. US20030215449A1

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; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/10/099,322
; PRIORITY FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 321
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-099-322-321
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Query Match      62.8%; Score 749; DB 17; Length 861;
Best Local Similarity 90.4%; Pred. No. 1.5e-225;
Matches 849; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 151 ATGGAACAGAGACCTTGAAGACCTTCCAGCATGCGAGGAAAGTTCCCCAGCGGACC 210
Db 7 ATGGAACAGAGACCTTGAAGACCTTCCAGCATGCGAGGAAAGTTCCCCAGCGGACC 66

Qy 211 CCGCAGAGCATTCCTACAGGACCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 270
Db 67 CCGCAGAGCATTCCTACAGGACCTCCCTACCTGTCATGTCAGAGGACAGTACCTC 126

Qy 271 TTCTGCAGTACTGGAACCCACAGGACACCCAAAGGCCCTCATCTTGTGTCCCATGGA 330
Db 127 TTCTGCAGTACTGGAACCCACAGGACACCCAAAGGCCCTCATCTTGTGTCCCATGGA 186

Qy 331 GCCGAGAGCAGTGGCCGCTATGAAGAGCTGGCTCGATGCTGATGGGCTGAGCCTG 390
Db 187 GCCGAGAGCAGTGGCCGCTATGAAGAGCTGGCTCGATGCTGATGGGCTGAGCCTG 246

Qy 391 CTGGTGTTCGCCACGACCATGTTGGCCACGACAGCGGAAGGGAGAGGATGGTAGTG 450
Db 247 CTGGTGTTCGCCACGACCATGTTGGCCACGACAGCGGAAGGGAGAGGATGGTAGTG 306

Qy 451 TCTGACTTCCACGTTTTCGTGAGGATGTTGTCAGCATGTCGATGTCGAAAGTGCTCAACCTTTGTG 510
Db 307 TCTGACTTCCACGTTTTCGTGAGGATGTTGTCAGCATGTCGATGTCGAAAGTGCTCAACCTTTGTG 366

Qy 511 TACCTCGGGCTTCCTGCTTTCCTTCTGGGGCACTTCCATGGGAGGCGCATCGCCATCCTC 570
Db 367 TACCTCGGGCTTCCTGCTTTCCTTCTGGGGCACTTCCATGGGAGGCGCATCGCCATCCTC 426

Qy 571 ACGGCCGACAGAGGCGGGCCACTTCGCGGCAATGCTACTATTTTCGCTCTGCTTCTT 630
Db 427 ACGGCCGACAGAGGCGGGCCACTTCGCGGCAATGCTACTATTTTCGCTCTGCTTCTT 486

Qy 631 GCCAACTCTGAATCTGCAACAACTTTCAAGTGCTTGTGCGAAAGTGCTCAACCTTTGTG 690
Db 487 GCCAACTCTGAATCTGCAACAACTTTCAAGTGCTTGTGCGAAAGTGCTCAACCTTTGTG 514

Qy 691 CTGCCAAACTTGTCCCTCGGGCCCATCGACTCCAGCGTGTCTCTCGGAATAAGACAGAG 750
Db 515 -----AG 516
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QY 751 GTCGACATTTATACTCAGACCCCTCTGATCTCCCGGGCAGGGCTGAAGTGTGCTTCGGC 810
Db |||||
QY 517 GTCGACATTTATACTCAGACCCCTCTGATCTCCCGGGCAGGGCTGAAGTGTGCTTCGGC 576
Db |||||
QY 811 ATCCCACTGCTGAATGCCGTCTCAGGGTGGAGCGCGCTCCCTCCCAAGTGACTGTGCC 870
Db |||||
QY 577 ATCCCACTGCTGAATGCCGTCTCAGGGTGGAGCGCGCTCCCTCCCAAGTGACTGTGCC 636
QY 871 TTCTCTGCTCTCAGGGCTCTCCGATCGCTATGTGACAGCAAAAGGGGCTTACCTGCTC 930
Db |||||
QY 637 TTCTCTGCTCTCAGGGCTCTCCGATCGCTATGTGACAGCAAAAGGGGCTTACCTGCTC 696
QY 931 ATGGAGTTAGCCCAAGAGCCAGGACAAGACTCTCAAGATTTATGAAGTGCCTTACCATGTT 990
Db |||||
QY 697 ATGGAGTTAGCCCAAGAGCCAGGACAAGACTCTCAAGATTTATGAAGTGCCTTACCATGTT 756
QY 991 CTCACAGAGGAGCTTCTGAAGTCAACCACTCCGCTTCCATGAATAAATGAATGTGGTGC 1050
Db |||||
QY 757 CTCACAGAGGAGCTTCTGAAGTCAACCACTCCGCTTCCATGAATAAATGAATGTGGTGC 816
QY 1051 TCTCAAGAGACAGCCAGGCAAGTCTGCTCCGCCACCC 1089
Db |||||
QY 817 TCTCAAGAGACAGCCAGGCAAGTCTGCTCCGCCACCC 855

RESULT 15
US-10-764-420-209
; Sequence 209, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-209

Query Match 56.0%; Score 667.2; DB 21; Length 912;
Best Local Similarity 83.2%; Pred. No. Ie-199;
Matches 759; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 181 ATGCCAGAGGAAAGTTCCCGAGGGCGGACCCCGAGAGCAATTCCTACAGGACCTCCCT 240
Db |||||
QY 241 CACCTGGTCAATGACAGCGGACAGTACTCTTCTGCGAGTACTGGAACCCACAGGCACA 300
Db |||||
QY 301 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCGGAGACAGTGGCGCTATGAAGAG 360
Db |||||
QY 121 CCCAAGGCCCTCATCTTTGTGTCCTCCATGGAGCTGGGGAACACTGTGGCGGTTATGATGAG 180
QY 361 CTGGCTCGGATGCTGATGGGCTGGACCTGCTGGTGTGTCGCCACAGCACCATGTTGGCCAC 420
Db |||||
QY 181 CTGGCTCATATGTTGAAGGGCTGGACATGCTGGTATTGTCCTCCATGACCATGTTGGCCAT 240
QY 421 GGACAGAGCGAAGGGGAGAGGATGGTGTGCTGACTTCCACGTTTTCGTGAGGGATGTG 480
Db |||||
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Db 241 GGGCAGAGTGAGGGAGAGAGGATGGTGGTGTGCGACTTCCAAAGTTTTTGTGCAGAGATGTG 300
QY 481 TTGCAGCATGTGGATTCCATGCGAGAAAGACTACCCCTGGGCTTCTGCTCTTCTCTGCGG 540
Db |||||
QY 301 CTGCAACAGGTGGACACATCCAGAGGACTACCCCGACGTCCCCATCTTCTCTCTGCGG 360
QY 541 CACTCCATGGAGGGCGCCATCGCCATCCTCACGGCCGACAGAGGGCGGGCCACTTTCGCC 600
Db |||||
QY 361 CACTCCATGGCGGTGCGCATCTCCATCCTAGTGGCTGACAGAGAGGCGCAACCTACTTTTCT 420
QY 601 GGCATGTGACTCATTTTCGCTCTGGTCTTTCGCCAATCTGAACTGCAACAACTTTTCAAG 660
Db |||||
QY 421 GGCATGTGCTGATTTTCACTCTGGTCTTCCCAATCCGGAATCTGCACTGCACTTTGAAG 480
QY 661 GTCCTTCTGCGAAAGTGTCTCAACTTTGTGTCGCAAACTTGTCCCTCGGSCCCATCGAC 720
Db |||||
QY 481 GTCCTTCTGCGAAACTGTCTCAATTTTGTCTGCGCAATATGACCTTGGGGCGCATTTGAC 540
QY 721 TCCAGCGTGTCTCTTCGGAATAAGACAGAGGTGACATTTTAACTCAGACCCCTCGATC 780
Db |||||
QY 541 TCCAGCGTGTCTCTTCGGAACAAGTGGAGGTTGACCTGTACAACTCTGACCCCACTCGTC 600
QY 781 TCCGGGCGAGGCTGAAGGTGTGCTTCGGCATCCAACTGCTGAATGCGCTCTCAGCGGTG 840
Db |||||
QY 601 TCCGAGCAGGGCTGAAGGTGTGCTTTGGCATACAGCTGCTGATGCTGCGCAAGAGTG 660
QY 841 GAGCGGCCCTCCCAAGCTGACTGTGSCCTTCTGCTGCTCCAGGGCTCTGCCGATCGC 900
Db |||||
QY 661 GAGCGAGCAATGCCAGGCTGACACTGCCATCTCTGCTGCGAGGTTCTGCTGACCGG 720
QY 901 CTATGTGACAGCAAAAGGGGCTTACCTGCTCATGGAGTTAGCCAGAGCCAGGACAAGACT 960
Db |||||
QY 721 CTTTGGCAGACAGCAAAAGGTGCTTACCTGCTCATGGAATCATCCCGAGCTCAGGACAAAACA 780
QY 961 CTCAGATTTTGAAGTGTGCTTACCATGTTCTCCAAAGGAGTTCCTGAAGTCAACCAAC 1020
Db |||||
QY 781 CTCAGATGTATGAAGTGTGCTTACCTGCTCCACAGGGAGGTTCCGGAAGTGAACCAAC 840
QY 1021 TCCGCTCTTCCATGAATAAATGAGTGTGCTCTCCAAAGGACAGCCAGCGAGGAACTGCG 1080
Db |||||
QY 841 TCCGCTCTTCCATGAAGTAAACTCGTGGTGTCTCACAGGATAGCAGCAGGAGTGGG 900
QY 1081 TCCGCCACCTCTGA 1092
Db |||||
QY 901 TGTCCACCTCTGA 912
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Job time : 796 secs

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